Title: Perfect score:

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Scoring table:

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BQ6890505 AGENCOURT BE797306 602256926
BG677068 AGENCOURT BQ677068 AGENCOURT BM810991 AGENCOURT BM810991 AGENCOURT BM810990 AGENCOURT BM820143 AGENCOURT BM920143 AGENCOURT BM920143 AGENCOURT BM920143 AGENCOURT BM920143 AGENCOURT BG182529 602725613 AW994476 RC3-BN003 BE747163 601577254 R51138 997146 RC3-BN003 BE747163 601577268 EB1825731 602059518 BR925696 601677393 BF55432 601677393 BF55432 601677393 BF55432 601677393 BF55432 601677393 BF55432 601677393 BF911515 AGENCOURT BQ0071202 AGENCOURT BC00936 601674206 BM9385 601674206 BM9385 60167421
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Email: cgapbs-r@mail.nih.gov
Tissue Produrement: Ash Alizadeh, John Byrd, M.D., Mike Grever,
Tissue Produrement: Ash Alizadeh, John Byrd, M.D., M.D., M.D., Louis M. Staudt, M.D., Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llni.gov/bbrp/image/image.html
Insert Length: 2499 Std Error: 0.00
Seq primer: -400P from Gibco
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cos611.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2073045 3',
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                     BI257580
BE795820
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BM690352 UI-E-CIO-
RS8841 y989d01.r1
BE383336 601298249
BE260495 6011298656
                                                                            May 17, 2003, 15:56:54 ; Search time 1090.13 Seconds (without alignments) 11900.029 Million cell updates/sec
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         5.1.5
Compugen Ltd.
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                                                                                                                       US-09-434-382-28_COPY_21800_22600
         GenCore version
Copyright (c) 1993 - 2003
                                                                                                                                                                                                                                                                                       Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                       nucleic search, using sw model
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Result No.

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                                                   BM690352 559 bp mRNA linear EST 28-FEB-2002 UI-E-CIO-aah-b-03-0-UI.rl UI-E-CIO Homo sapiens cDNA clone UI-E-CIO-aah-b-03-0-UI 5', mRNA sequence.
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Bonaldo, M.F., Lennon, G. and Soares, M.B.
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Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 TATTAGCTCCTCAAAAGCAAAGCAGAGAAAAAAATTTCTGCAGTTGCTTCTTGGTCCT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181 GTCCAAAGCAGACATCAGCCTCTGAACCATCAGCAGTCTTCCTAGTGGCAGTGACTCTCT 240
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Pred. No. 1.6e-62;
1; Mismatches 1; Indels
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                                         /organism="Homo sapiens"
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High quality sequence stop: 351.
Location/Qualifiers
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Best Local Similarity 99.4%;
Matches 354; Conservative
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1 (bases 1 to 48).

1 (hases 1 to 48).

M., Hullier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and Wilson, R.

The Washld-Merck EST Project
Unpublished (1995)
Fax: 319 335 9565
Email: msoares@blue.weeg.uiowa.edu
Tissue Procurement: Dr. Gregg Hageman
cDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa
clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com).
Seg primer: M13 Reverse.
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IMAGE:40931 5' similar to SP:YK59 YEAST P36159 HYPOTHETICAL
PROTEIN IN SIS2-MTDI INTERGENIC ; mRNA sequence.
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89.7%; Pred. No. 4.1e-20;
iive 1; Mismatches 17
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BE260495.1 GI:9131807
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 664)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
        Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1800
Email: estewatson.wustl.edu
Insert Size: 1777
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 1777 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                338 AGIGGCAGIGACTCTTCTTCTTCTTCTGCAGCCCCGACACGTCTCTGCTACTGGAC 397
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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ilarity 89.1%; Pred. No. 5.6e-20;
Conservative 1; Mismatches 18
                                                                                                                                                                                                                   1. .482
/organism="Homo sapiens"
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Seq primer: M13RP1
High quallicy sequence stop: 387.
Location/Qualifiers
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Mammalia; Eutheria, Primates, Catarrhini, Hominidae, Homo.

    (bases 1 to 676)

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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCM1/6 row: d column: 01
High quality sequence stop: 672.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov Plate: LLCM31s row: a column: 13
High quality sequence stop: 662.
Location/Qualifiers
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National Institutes of Health, Mammalian Gene Collection (MGC)
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/note="Organ: brain; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5; adaptor: GGGACGAG(G). Library constructed by Ling Hong in the laboratory of Garald M Rubin (University of california, Berkeley) using ZAP-CDNA synchesis kit (Strategene) and Superscript II RT (Life Technologies).

Note: this is a NIH_MGC Library."
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/tissue_type="neuroblastoma"
/lab host="HIOB (phage-resistant)"
/note="Organ: brain, Vector: pDTB7; Site_1: XhoI; Site_2:
BCORI, cDNA made by oligo-dT priming. Directionally
cloned into BCORI/XhoI sites using the following 5'
adaptor: GGCACGAG(0). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-CDNA synthesis kit
(Strategene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
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MNH-MGC http://mgc.nci.nih.gov/.
National institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
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89.1%; Pred. No. 5.2e-20;
ive 1; Mismatches 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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                                                                                                                                                                                                                                                                                                                                                 Matches 156; Conservative
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 698)
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCM807 row: f column: 23
High quality sequence stop: 389.
Location/Qualifiers
                                                                                                                                                                                                             338 AGTGGCAGTGACTCTTCTTTTTTTTTTTGCAGCCCCGACACGTCTCTGCTACTGGAC 397
                                                                                                                                                                                                                                                                                                                                                                                                                TGTGGTGAGGGCACRTTTGGGCAGCTGTGCCGTCATTACGGAGACCAGGTGGACAGGGGTC 457
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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Score 145.8; DB 10; Length 692;
                                                                                                         Indels
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                                                    Pred. No. 5.2e-20;
                                                                                                    1; Mismatches
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/db_xref="taxon:9606"
/clone="IMAGE:3946774"
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
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18.2%;
89.1%;
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Homo sapiens
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/db xref="taxon:9606"
/clone="myAgEs:434981"
/clone="myAgEs:434981"
/clone=lib="NHH MGC 41"
/tissue_type="amelanotic melanoma, cell line"
/tab_host="DH10B (phage-resistant)"
/note="lorgan: skin; Vector: pOTP7; Site 1: XhoI; Site 2:
ECORI; cDNA made by oligo-dT priming. Directionally cloned
into ECORI/XhoI sites using the following 5' adaptor:
GGCAGGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
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                                                                                                                                                                                                  BM009099 726 bp mRNA linear EST 30-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.lln.gov
Plate: LLCM1912 row: o column: 14
High quality sequence stop: 636.
Location/Qualifiers

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1. 726
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
 457
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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                                    68 TGTGGTGAGGCACGTTTGGCCAGCTGTGCCGTCATTACGGAGACCAGGTGGACAGGGTC
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TGTGGTGAGGGCACRTTTGGGCAGCTGTGCCGTCATTACGGAGACCAGGTGGACAGGGTC
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                                                                                          128 CTGGGCACCCTGGCTGCTGTGTTTTGTGTCCCACCTGCACGCAGATCACCACACGG 182
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Best Local Similarity 89.1%; Pred. No. 5.1e-20;
Matches 156; Conservative 1; Mismatches 18
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RESULT

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BE795820 761 bp mRNA linear EST 20-SEP-2000 001590856F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3945085 5',
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BI257580 756 bp mRNA linear EST 17-JUL-2001
602967138F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:5106944 5',
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/clone="IMAGE:5106944"

/clone="IMAGE:5106944"

/clone="ID="MAIH MGC_12"

/tissue type="cervical carcinoma cell line"

/lab_host="DH10B"

/note="Organ: cervix, Vector: pCMV-SPORT6; Site 1: NotI;

Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.

Average insert size 1.4 kb. Library prepared by Life
                                                                                                                                                                                                                       Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mamalai Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (Dasas 1 to 756)
NMH-MGC http://mgc.nci.nih.gov/.
NMH-MGC http://mgc.nci.nih.gov/.
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Incyte Genomics, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.W.A.G.E. Consortium/LLNL at:
http://image.llnh.gov. k column: 09
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Pred. No. 5.1e-20;
1; Mismatches 18; Indels 0;
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Location/Qualifiers
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                                                                                                                             BI257580.1 GI:14813096
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89.1%;
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AGENCOURT_8208640 NIH_MGC_102 Homo sapiens CDNA clone IMAGE:6254562
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1 (bases 1 to 874)

NIH-MCC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                               CDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: More distribution can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov Plate: LLCM802 row: p column: 14
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89.1%; Pred. No. 5.1e-20;
iive 1; Mismatches 18
                                                                                                                                                                                                                                                                                                                                                                                                                                               'organism="Homo sapiens"
                            Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
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Location/Qualifiers
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BQ674529
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KEYWORDS
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/clone_lib="NIH MGC_102"
/tissue_type="epidermoid carcinoma, cell line"
/lab_host="bh108 (phage-resistant)"
/note="Organ: salivary gland; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5; daptor: GGGACGAG(G). Library constructed
by Ling Hong in the laboratory of Gerald M. Rubin
(University of California, Berkeley) using ZAP-cDNA
synthesis kit (Stratagene) and Superscript II R (Life
Technologies). Note: this is a NIH_MGC Library."
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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/clone lib="NIH MGC 110"
/tissue_type="ductal carcinoma, cell line"
/lab_host="PH108 (phage-resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. 4.9e-20;
1; Mismatches 18; Indels
column: 19
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/db xref="taxon:9606"
                                                                                                                             /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:6254562"
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                              High quality sequence stop: 6
Location/Qualifiers
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Length 884;

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Conservative
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Best Local Similarity
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                                              Matches 156;
      Query Match
Best Local 9
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DEFINITION
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/tissue_type="neuroblastoma"
/tab host="DH108 (phage-resistant)"
/note="Organ: brain; Vector: poTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAGG(G). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-CDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH-MGC Library."
/note="Organ: pancreas; Vector: pOTB7; Site_1: XhoI; Ste_2: EcoR1; cDNA made by oligo-dT priming.
Directionally cloned into EcoR1/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagnel) and Superscript II RT (Life Technologies).

Note: this is a NIH MGC Library.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 884)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Colone distribution: MGC clone distribution and Colone distribution and the LLCM1A.B. Consortium/LLNL at: image.llnl.gov Plate: LLCM176 row: d column: 01
                                                                                                                                                                                                                                                                                                                                                                                                                        338 AGTGGCAGTGACTCTCTTCTCTTCTGCAGCCCCGACACGTCTCTGCTACTGGAC 397
                                                                                                                                                                                                                                                                                                                                       230 ATTGGAAATGTCAGTGCCACACTTGTCAACATAAGCCCCGGACACGTCTCTGCTACTGCTACTGGAC 289
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                               398 TGTGGTGAGGCCACRTTTGGGCAGCTGTGCCGTCATTACGGAGACCAGGTGGACAGGGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTGGGCACCCTGGCTGTGTGTGTGTCCCACCTGCACGAGATCACCACACGG 512
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Pred. No. 4.9e-20;
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:9606"
/clone="IMAGE:3503184"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BG519751.1 GI:13515513
                                                                                                                                                                                                                             Query Match
Best Local Similarity 89.1%;
Matches 156; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                      mRNA sequence.
BG519751
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TITLE
JOURNAL
COMMENT
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KEYWORDS
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Focal: cDNa made by oligo-dT priming Directionally
cloned into EcoRI/XhoI sites using the following 5;
adaptor: GGCACGAG(G). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using 2AP-CDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
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10 Dates 1 to 915)

10 NIH-MGC http://mgc.nci.nih.gov/.

11 Institutes of Health, Mammalian Gene Collection (MGC)

12 Contact: Robert Strausberg, Ph.D.

13 Contact: Robert Strausberg, Ph.D.

14 Contact: Gapbs-r@mail.nih.gov

15 Contact: Gapbs-r@mail.nih.gov

17 Stsue Procurement: ATC.

18 Contact: Capps-rganil.nih.gov

19 Contact: Capps-rganil.nih.gov

10 Contact: Capps-rganil.nih.gov

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18 Contact: Capps-rganil.nih.gov
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18.2%; Score 145.8; DB 1.89.1%; Pred. No. 4.9e-20; vative 1; Mismatches 18
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Pred. No. 4.9e-20;
1; Mismatches 18
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                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1. (Dases 1 to 915)

2. NIH-MGC http://mgc.nci.nih.gov/.

3. NIH-MGC http://mgc.nci.nih.gov/.

3. NIH-MGC http://mgc.nci.nih.gov/.

4. Ontact: Robert Strausberg, Ph.D.

5. Email: cgapbs-remail.nih.gov

6. Contact: Robert Strausberg, Ph.D.

7 issue Procurement: DCTD/DTP

7 cDNA Library Preparation: Rubin Laboratory

7 cDNA Library Preparation: Rubin Laboratory

7 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

8 DNA Sequencing by: Agencourt Bioscience Corporation

7 clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

8 high quality sequence stop: 720.

9 Location/Qualifiers
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AGENCOURT_8071095 NIH_MGC_112 Homo sapiens cDNA clone IMAGE:6089876
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458 CTGGGCACCCTGGCTGCTGTTTGTGTCCCACCTGCACGCAGATCACCACGC 512
                         533 CTGGGCACCCTGGCTGCTGTGTTTGTGTCCCACCTGCACGCAGATCACCACACGG 587
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VERSION
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AUTHORS
TITLE
JOURNAL
COMMENT
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Search completed: May 17, 2003, 18:18:28

Job time : 1096.13 secs

Sequence 379, Appl Sequence 296, Appl Sequence 296, Appl Sequence 261, Appl Sequence 211, Appl Sequence 255, Appl Sequence 256, Appl Sequence 144, Appl Sequence 144, Appl Sequence 1312, Appl Sequence 1146, Appl Sequence 1156, Appl Sequence 1156, Appl Sequence 1156, Appl Sequence 1697, Appl Sequence 16987, Appl Sequence 16997, Appl Sequence 4, Appli Sequence 4, Appli Sequence 4, Appli Sequence 4, Appli

Sequence 402, App Sequence 402, App Sequence 312, App

Sequence 312,

ALIGNMENTS

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APPLICANT: Tavtigian, Sean V.
APPLICANT: Tavtigian, Sean V.
APPLICANT: Tavtigian, Bavid H.F.
APPLICANT: Simard, Jacques
APPLICANT: Simard, Jacques
APPLICANT: Simard, Jacques
TITLE CANTER Rommens, Johanna M.
APPLICANT: Myriad Genetics, Inc.
TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility
TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes
TITLE OF INVENTION: Cene and a Paralog and Orthologous Genes
TITLE OF INVENTION: Cene and a Paralog and Orthologous Genes
TITLE OF INVENTION WIMBER: US/09/988,626
CURRENT APPLICATION NUMBER: US 60/107,468
PRIOR PILING DATE: 1999-11-06
PRIOR PILING DATE: 1999-11-05
PRIOR PILING DATE: 1999-11-05
NUMBER: OF SEQ ID NOS: 240
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 28
LENGTH: 26664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PAME/KEY: misc feature

LOCATION: (910)...(13104)

COTER INFORMATION: exon 1: 910-1154; exon 2: 1736-1786; exon 3:

LOCATION: (910)...(13104)

COTHER INFORMATION: exon 6: 5582-5650; exon 7: 7075-7194; exon 8:

OTHER INFORMATION: 8186-8244; exon 9: 12878-12936; exon 10:

OTHER INFORMATION: 13032-13104;

NAME/KEY: misc feature

LOCATION: (13756)...(22917)

OTHER INFORMATION: exon 11: 13756-13868; exon 12: 15283-15378; exon 7: 707E-11000AATION: 13. 16278-16416; exon 14: 16498-16583; exon 15: 0THER INFORMATION: 13: 16278-16416; exon 14: 16498-16583; exon 15: 0THER INFORMATION: 22172-22310; exon 18: 22879-22917

NAME/KEY: misc_feature
Sequence 28, Application US/09988626; Publication No. US20030044959A1; GENERAL INFORMATION:
    3253
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499
416
559
478
513509
                                                     1578
1182
2454
2454
2664
512
2005
8801
17056
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653
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ORGANISM: Homo sapiens
FEATURE:
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Sequence 225, App
Sequence 223, App
Sequence 223, App
Sequence 3, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 20, Appl
Sequence 20, Appl
Sequence 221, Appli
Sequence 221, Appli
Sequence 221, Appli
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Sequence 1517, Ap
Sequence 1518, Ap
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                                                                                       May 17, 2003, 17:27:39 ; Search time 101.551 Seconds (without alignments) 10174.595 Million cell updates/sec
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Sequence
Sequence
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1: /cgn2_6/ptodata/1/pubpna/USO7 PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/PCT NEW PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/USO6 NEW PUB.seq:*
4: /cgn2_6/ptodata/1/pubpna/USO6 NEW PUB.seq:*
5: /cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*
6: /cgn2_6/ptodata/1/pubpna/USO8_NEW PUB.seq:*
7: /cgn2_6/ptodata/1/pubpna/USO8_NEW PUB.seq:*
9: /cgn2_6/ptodata/1/pubpna/USO8_NEW PUB.seq:*
9: /cgn2_6/ptodata/1/pubpna/USO9_NEW PUB.seq:*
10: /cgn2_6/ptodata/1/pubpna/USO9_NEW PUB.seq:*
11: /cgn2_6/ptodata/1/pubpna/USO9_NEW PUB.seq:*
12: /cgn2_6/ptodata/1/pubpna/USO9_NEW PUB.seq:*
13: /cgn2_6/ptodata/1/pubpna/USO0_NEW PUB.seq:*
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US-10-092-154-1518
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US-09-988-687-23
US-09-988-687-3
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Perfect score:
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OTHER INFORMATION: exon 19: 23045-23154; exon 20: 23795-23895; exon OTHER INFORMATION: 21: 23973-24093; exon 22: 24354-24432; exon 23: OTHER INFORMATION: 25026-25170; exon 24: 25812-26036; polyadenylation OTHER INFORMATION: signal: 26447-26452

NAME/KEY: variation
LOCATION: (826)..(23879)
OTHER INFORMATION: positions 826 and 23180 is G or C; y at OTHER INFORMATION: is C or T; n at position 13128 is t or tgat; r at COTHER INFORMATION: is C or T; n at a 23879 is A or G.
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US-09-988-626-28
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APPLICANT: Tavidain, Sean V.
APPLICANT: Tavidain, Sean V.
APPLICANT: Tavidain, Sean V.
APPLICANT: Simard, Jacques
APPLICANT: Simard, Jacques
APPLICANT: Rommens, Jacques
APPLICANT: Rommens, Johanna M.
APPLICANT: Rommens, Johanna M.
APPLICANT: Myriad Genetics, Inc.
TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility
TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes
FILE REFERENCE: 2318-258
CURRENT APPLICATION NUMBER: US/09/988,687
CURRENT FILING DATE: 2001-11-20
PRIOR PLING DATE: 2000-05-05
PRIOR PLING DATE: 1999-11-06
PRIOR PLING DATE: 1999-11-06
PRIOR PLING DATE: 1999-11-05
NUMBER OF SEQ ID NOS: 240
SOFTWARE: PatentIn Ver. 2.0
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INFORMATION: exon 19: 23045-23154; exon 20: 23795-23895; exon INFORMATION: 21: 23973-24093; exon 22: 24354-24432; exon 23: INFORMATION: 25026-25170; exon 24: 25812-26036; polyadenylation INFORMATION: signal: 26447-26452
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INFORMATION: s at positions 826 and 23180 is G or C; y at INFORMATION: positions 1914, 5568, 7165, 16431, 1857 and 20486
INFORMATION: is C or T; n at position 13128 is t or tgat; r at INFORMATION: positions 22211 and 23879 is A or G.
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100.0%; Pred. No. 6.4e-23
:ive 0; Mismatches 0
; Sequence 28, Application US/09988687; Publication No. US20030045704A1; GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 801; Conservative
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NAME/KEY: misc feature
LOCATION: (910)..(13104)
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ORGANISM: HOMO
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Score 145.8; DB 9; Pred. No. 6.8e-34; 1; Mismatches 18;

Length 2481;

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1486 ATTCGAAATGTCAGTGCCACACTTGTCAACATAÁGCCCCGACACGTCTCTGCTACTGGAC 1545
                                                                                                                              338 AGTGGCAGTGACTCTCTTCTTCTTCTTCTGCAGCCCCGACACGTCTCTGCTACTGGAC 397
                                                       Query Match
Best Local Similarity 89.1%;
Matches 156; Conservative
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US-09-988-687-1
     (1) .. (2478)
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US-09-988-626-225
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   , LOCATION: (;
US-09-988-626-1
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Publication No US20030044959A1

GENERAL INRORMATION:

APPLICANT: Tavtigian, Sen V.

APPLICANT: Tavtigian, Sen V.

APPLICANT: Tavtigian, Sen V.

APPLICANT: Tavtigian, Sen V.

APPLICANT: APPLICANT: Normens, Johanna M.

TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility

TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes

TITLE OF INVENTION: US/09/988,626

CURRENT APPLICATION NUMBER: US/09/988,626

CURRENT FILING DATE: 2001-01-20

PRIOR APPLICATION NUMBER: US 60/107,468

PRIOR FILING DATE: 1998-11-06

PRIOR APPLICATION NUMBER: 09/434,382

PRIOR FILING DATE: 1999-11-05

NUMBER OF SEQ ID NOS: 240

SOFTWARE: PATENTIN VETE: 2.0
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NAME/KEY: CDS
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LENGTH: 2481
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APPLICANT: Tavidian, Sean V.
APPLICANT: Tavidian, Sean V.
APPLICANT: Tavidian, Sean V.
APPLICANT: Tavidian, Sand H.F.
APPLICANT: Simard, Jacques
APPLICANT: Romens, Johanna M.
APPLICANT: Romens, Johanna M.
APPLICANT: Myriad Genetics, Inc.
TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility
TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes
TITLE OF INVENTION UMBER: US/09/988,687
CURRENT FILING DATE: 2000-05-05
PRIOR PILING DATE: 2000-05-05
PRIOR PILING DATE: 1999-11-06
PRIOR PILING DATE: 1999-11-06
PRIOR PILING DATE: 1999-11-05
PRIOR FILING DATE: 1999-11-05
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398 TGTGGTGAGGCCACRTTTGGGCAGCTGTGCCGTCATTACGGAGACCAGGTGGACAGGGTC
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Pred. No. 6.8e-34;
1; Mismatches 18
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; Publication No. US20030044959A1
                                                                                                                                                                                                                                                                                                                        Sequence 1, Application US/09988687
Publication No. US20030045704A1
GENERAL INFORMATION:
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89.1%;
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO.
LENGTH: 2481
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Matches 156; Conservative
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; LOCATION: (1)
US-09-988-687-225
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US-09-988-626-223
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APPLICANT: Tavitgian, Sean V.
APPLICANT: Tavitgian, Sean V.
APPLICANT: Tavitgian, Jacque H.F.
APPLICANT: Teng, David H.F.
APPLICANT: Simard, Jacques
APPLICANT: Simard, Jacques
APPLICANT: Romenens, Johanna M.
APPLICANT: Romenens, Johanna M.
APPLICANT: Myriad Genetics, Inc.
TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility
TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes
FILE REFERENCE: 2318-258
CURRENT APPLICATION NUMBER: US/09/988,626
CURRENT FILING DATE: 2000-05-05
PRIOR PLILING DATE: 2000-05-05
PRIOR PLILING DATE: 1998-11-06
PRIOR PLILING DATE: 1998-11-06
PRIOR PLILING DATE: 1998-11-05
NUMBER OF SEQ ID NOS: 240
SOFTWARE: Patentin Ver. 2.0
SEG ID NO 225
LENGTH: 2892
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APPLICANT: Tavidian, Sean V.
APPLICANT: Teng, David H.F.
APPLICANT: Simard, Jacques
APPLICANT: Simard, Jacques
APPLICANT: Rommens, Johanna M.
APPLICANT: Rommens, Johanna M.
APPLICANT: Myriad Genetics, Inc.
TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes
TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes
TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes
CURRENT FILING DATE: 2001-11-20
PRIOR PLILNG DATE: 2001-05-05
PRIOR PLLING DATE: 1998-11-06
PRIOR PLLING DATE: 1998-11-06
PRIOR FILING DATE: 1999-11-05
PRIOR FILING DATE: 1999-11-05
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Pred. No. 7.5e-34;
1; Mismatches 18; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 225, Application US/09988687; Publication No. US20030045704A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 89.1%;
Matches 156; Conservative
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 225
LENGTH: 2892
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ORGANISM: Gorilla gorilla
FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; LOCATION: (1)..(2478)
US-09-988-626-225
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GENERAL INVERTATION:
APPLICANT: Tartigian, Sean V.
APPLICANT: Tartigian, Sean V.
APPLICANT: Tartigian, Jacques
Samard, Jacques
APPLICANT: Ramanens, Jacques
APPLICANT: Rommens, Jacques
APPLICANT: Rommens, Jacques
TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility
TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes
FILE REFERENCE: 2318-258
CURRENT APPLICATION NUMBER: US/09/988,626
CURRENT PAPLICATION NUMBER: US/0564,805
PRIOR FILING DATE: 2001-11-20
PRIOR FILING DATE: 1998-11-06
PRIOR FILING DATE: 1998-11-05
NUMBER OF SEQ ID NOS: 240
SEQ ID NO 223
LENGTH: 2908
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                                                                            DB 9;
                                                                         Score 145.8; DB 9
Pred. No. 7.5e-34;
                                                                                                                             1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 223, Application US/09988626; Publication No. US20030044959A1; GENERAL INFORMATION:
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US-09-988-687-223
; Sequence 223, Application US/09988687
                                                                         Query Match
Best Local Similarity 89.1%;
Matches 156; Conservative
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ORGANISM: Pan troglodytes
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Similarity
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                            APPLICANT: Tavtiglan, Sean V.
APPLICANT: Tavtiglan, Sean V.
APPLICANT: Tavtiglan, David H.F.
APPLICANT: Tavtiglan, David H.F.
APPLICANT: Simard, Jacques
APPLICANT: Simard, Jacques
APPLICANT: Rommens, Johanna M.
APPLICANT: Rommens, Johanna M.
APPLICANT: Rommens, Johanna M.
APPLICANT: Myriad Genetics, Inc.
ITILE OF INVENTION: Gene and a Paralog and Orthologous Genes
ITILE OF INVENTION: Gene and a Paralog and Orthologous Genes
FILE REFERENCE: 2118-258
CURRENT APPLICATION NUMBER: US/09/988,687
CURRENT APPLICATION NUMBER: US 60/107,468
PRIOR FILING DATE: 1998-11-05
PRIOR FILING DATE: 1998-11-05
PRIOR FILING DATE: 1999-11-05
PRIOR FILING DATE: 1999-11-05
NUMBER OF SEQ ID NOS: 240
SCOUTHARE: Patentin Ver. 2.0
SEQ ID NO 223
LENGTH: 2908
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 3, Application US/0998626;
Publication No. US200300449591
GENERAL INFORMATION:
APPLICANT: Tavtigian, Sean V.
APPLICANT: Tavtigian, David H.F.
APPLICANT: Tavtigian, Jacques
APPLICANT: Simard, Jacques
APPLICANT: Simard, Johanna M.
TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility
TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility
TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes
FILE REFERENCE: 2318-258
CURRENT APPLICATION NUMBER: US/09/988,626
CURRENT FILING DATE: 2000-05-05
PRIOR FILING DATE: 2000-05-05
PRIOR FILING DATE: 1999-11-06
PRIOR FILING DATE: 1999-11-06
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 3
LENGTH: 2958
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Pred. No. 7.5e-34;
1; Mismatches 18;
Publication No. US20030045704A1
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Best Local Similarity 89.1%;
Matches 156; Conservative
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ORGANISM: Homo sapiens
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US-09-988-687-223
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APPLICANT: Tavidian, Sean V.
APPLICANT: Simard, Joaques
APPLICANT: Rommens, Joaques
APPLICANT: Rommens, Joaques
APPLICANT: Myriad Genetics, Inc.
TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes
FILE REFERENCE: 2318-258
CURRENT APPLICATION NUMBER: US/09/988,687
FILE REFERENCE: 2001-11-20
PRIOR FILING DATE: 2001-01-20
PRIOR PELING DATE: 1999-11-06
PRIOR FILING DATE: 1999-11-06
PRIOR FILING DATE: 1999-11-05
NUMBER OF SEQ ID NOS: 240
SOFTWARR: PACENTIN VET. 2.0
SOFTWARR: PACENTIN VET. 2.0
SOFTWARR: PACENTIN VET. 2.0
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                                                                                                                                                            Length 2958;
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NAME/KEY: misc_feature

LOCATION: (51)..(2531)

LOCATION: (51)...(2531)

US-09-988-666-3
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LOCATION: (51)..(2531)
OTHER INFORMATION: coding sequence as in SEQ ID NO:1
                                                                                                                                                         Score 145.8; DB 9;
Pred. No. 7.6e-34;
1; Mismatches 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 3, Application US/09988687; Publication No. US20030045704A1; GENERAL INFORMATION:
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ilarity 89.1%;
Conservative
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Matches 156; Conservative
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SEQ ID NO 20
LENGTH: 139
TYPE: DNA
ORGANISM: Homo sapiens
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Matches 128; Conserv
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LENGTH: 2470
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                                                     Sequence 20, Application US/09988687

Publication No. US20030045704A1

GENERAL INFORMATION:
APPLICANT: Tavtigian, Sean V.
APPLICANT: Tavtigian, Sean V.
APPLICANT: Tavtigian, Joaques
APPLICANT: Tavtigian, Carones
APPLICANT: Rommens, Johanna M.
TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility
TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes
FILE REFERENCE: 2318-258
CURRENT APPLICATION NUMBER: US/09/988,687
CURRENT FILING DATE: 2001-11-20
FRIOR APPLICATION NUMBER: 09/564,805
FRIOR APPLICATION NUMBER: 09/564,805
FRIOR FILING DATE: 1998-11-06
FRIOR APPLICATION NUMBER: 09/544,805
FRIOR FILING DATE: 1999-11-06
FRIOR APPLICATION NUMBER: 09/544,805
FRIOR FILING DATE: 1999-11-06
FRIOR APPLICATION NUMBER: 09/434,382
FRIOR FILING DATE: 1999-11-05
FRIOR SEQ ID NOS: 240
FRIOR SEQ ID NOS: 240
FRIOR SEQ ID NOS: 240
FRIOR SEQ ID NOS: 220
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                                ; Sequence 20, Application US/09988626
; Publication No. US20030044959A1
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Best Local Similarity 99.3%;
Matches 138; Conservative
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| LOCATION: (1)..(139)

| OTHER INFORMATION: exon 17

US-09-988-626-20
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US-UN-988-beb-21,
Squence 221, Application US/09988626

Publication No. US200300449991

GRNERAL INFORMATION:
APPLICANT: Tavtigian, Sean V.
APPLICANT: Tavtigian, Sand H.F.
APPLICANT: Romens, Johanna M.
APPLICANT: Romens, Johanna M.
APPLICANT: Myriad Genetics, Inc.
TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility
TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes
FILE REFERENCE: 2318-258
CURRENT APPLICATION NUMBER: US/09/988,626
CURRENT FILING DATE: 2000-11-20
PRIOR PAPLICATION NUMBER: US 60/107,468
PRIOR PILING DATE: 1998-11-06
PRIOR APPLICATION NUMBER: 09/434,382
PRIOR FILING DATE: 1998-11-05
PRIOR PILING DATE: 1999-11-05
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                                                                                                                                                     Length 139;
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Pred. No. 1.6e-20;
0; Mismatches 43;
                                                                                                                                                       DB 9;
                                                                                                                                                     Score 138.6; DB 9,
Pred. No. 1.8e-32;
1; Mismatches 0;
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                                                                                                                                                     Query Match
Best Local Similarity 99.3%;
Matches 138; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 GCACGCAGATCACCACACG 139
PEATURE:
NAME/KEY: misc feature
LOCATION: (1)...(139)
OTHER INFORMATION: exon 17
US-09-988-687-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Ver. 2.0
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US-09-988-626-221
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1571 GCAGCCTCACGGCTGTTTGTGTCCCCACCTGCACGCCGACCACCACGG 1621

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APPLICANT: Simard, Jacque n.s.
APPLICANT: Somens, Johanna M.
APPLICANT: Rommens, Johanna M.
APPLICANT: Rommens, Johanna M.
APPLICANT: Rommens, Johanna M.
TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility
TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes
FILE REFERENCE: 2318-258
CURRENT APPLICATION NUMBER: US/09/988,687
CURRENT FILING DATE: 2001-11-20
PRIOR APPLICATION NUMBER: US 60/107,468
PRIOR APPLICATION NUMBER: 09/434,382
PRIOR FILING DATE: 1998-11-06
PRIOR APPLICATION NUMBER: 09/434,382
PRIOR FILING DATE: 1999-11-05
NUMBER OF SEQ ID NOS: 240
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 221
LENGTH: 2470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1511 GAGAAGGCACTTTTGGGCAGTTGTGCCGTCATTACGGACAGAAATAGACCGAGTCTTAT 1570
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CURRENT APPLICATION: NUMBER: US/10/092,154
CURRENT FILING DATE: 2002-03-07
NUMBER OF SEQ ID NOS: 2003
Prior Application removed - See File Wrapper or Palm SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1517
LENGTH: 1152
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Sequence 1517, Application US/10092154

Publication No. US20030054375A1

GENERAL INFORMATION:
                                                                 Sequence 221, Application US/09988687
Publication No. US20030045704A1
                                                                                                         GENERAL INFORMATION:
APPLICANT: Tavtigian, Sean V.
APPLICANT: Teng, David H.F.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA ORGANISM: Mus musculus
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Best Local Similarity
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Best Local Similarity
Matches 128; Conserv
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US-09-988-687-221
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   Gaps
                                                                 TITCAACAGAGGCTGTGGCCACACTCAATCTGCATGGTCAGATTCATTGTTAGGACTAAA 77
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0; Mismatches 108;
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   Conservative
   Matches 104;
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TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
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       SOFTWARE: Pater
SEQ ID NO 28
LENGTH: 26664
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Sequence 225, App
Sequence 223, Appli
Sequence 30, Appli
Sequence 201, Appli
Sequence 14, Appl
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                                                                                                                                                         May 17, 2003, 15:56:54 ; Search time 45.0714 Seconds (without alignments) 5450.193 Million cell updates/sec
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Sequence 1, Al
Sequence 261,
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Sequence 1, Ar
Sequence 10, 7
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Sequence 17,
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/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
/cgn2_6/ptodata/2/ina/6A_COMB.seq:*
/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
                   GenCore version 5.1.5
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-564-805-223
US-09-564-805-3
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US-09-461-697-261

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US-09-244-796-17

US-09-889-718-1

US-09-889-718-1

US-09-883-768-10

US-09-883-768-10

US-09-883-768-10

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Listing first 45 summaries
                                                                                                              nucleic search, using sw model
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length: 2000000000
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ALIGNMENTS

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JUNEARLY INFORMATION:
APPLICANT: Tavidgan, Sean V.
APPLICANT: Tavidgan, Sean V.
APPLICANT: Tavidgan, Sean V.
APPLICANT: Start of Javid H.F.
APPLICANT: Sommens, Johanna M.
APPLICANT: Myriad Genetics, Inc.
TITLE OF INVENTION: Cromosome 17p-Linked Prostate Cancer Susceptibility
TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes
TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes
FILE REFERENCE: 2318-28
CURRENT APPLICATION NUMBER: US 60/107,468
FRIOR APPLICATION NUMBER: US 60/107,468
FRIOR APPLICATION NUMBER: 09/434,382
FRIOR FILING DATE: 1999-11-05
  Chromosome 17p-Linked Prostate Cancer Susceptibility Gene and a Paralog and Orthologous Genes
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                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
18.2%; Score 145.8; DB 4;
Best Local Similarity 89.1%; Pred. No. 3.8e-34;
Matches 156; Conservative 1; Mismatches 18;
TITLE OF INVENTION: Chromosome 17p-Linked P TITLE OF INVENTION: Gene and a Paralog and FILE OF INVENTION: Gene and a Paralog and FILE OF INVENTION: Gene and a Paralog and CHROMER APPLICATION NUMBER: US/09/564,805 PRIOR APPLICATION NUMBER: US 60/107,468 PRIOR PILING DATE: 1998-11-06 PRIOR APPLICATION NUMBER: 09/434,382 PRIOR FILING DATE: 1999-11-05 NUMBER OF SEQ ID NOS: 240 SOFTWARE: Patentin Ver. 2.0
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; Patent No. 6333403
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                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Homo sapiens
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; LOCATION: (1)..(2478)
US-09-564-805-1
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; LOCATION: (1)..(2478)
US-09-564-805-225
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                                                100.0%; Score 800.6; DB 4; Length 26664; 100.0%; Pred. No. 7.6e-232;
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US-09-564-805-1
Sequence 1, Application US/09564805
; Patent No. 6333403
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Teng, David H.F.
Simard, Jacques
Rommens, Johanna M.
Myriad Genetics, Inc.
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                                                                    Best Local Similarity 100.
Matches 801; Conservative
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APPLICANT: Tavtigian
APPLICANT: Teng, Dav
APPLICANT: Rommens,
APPLICANT: Rommens,
APPLICANT: Myriad Ge
        US-09-564-805-28
                                                   Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 223, Application US/09564805

Patent No. 6333403

GENERAL INFORMATION:
APPLICANT: Tavtigian, Sean V.
APPLICANT: Tavtigian, Sean V.
APPLICANT: Tavtigian, Johanna M.
APPLICANT: Tavtigian, Graques
APPLICANT: Tavtigian, Graques
APPLICANT: Myriad Genetics, Inc.
APPLICANT: Without Myria Genetics, Inc.
TITLE OF INVENTION: Gradues
CURRENT APPLICATION NUMBER: US/09/564,805
CURRENT FILING DATE: 1998-11-05
PRIOR APPLICATION NUMBER: US/41.382
PRIOR APPLICATION NUMBER: US/41.382
NUMBER OF SEQ ID NOS: 240
SEQ ID NO 223
LENGTH: 2908
AUTH APPLICATION NUMBER: DS/41.382
AUTHOR APPLICATION NUMBER: US/41.382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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APPLICANT: Tang, David H.F.
APPLICANT: Simard, Jacques
APPLICANT: Simard, Jacques
APPLICANT: Romans, Johanna M.
APPLICANT: Romans, Johanna M.
TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility
TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes
FILE REFERENCE: 2318-258
CURRENT APPLICATION NUMBER: US/09/564,805
CURRENT FILING DATE: 2000-05-05
1486 ATTCGAAATGTCAGTGCCACACTTGTCAACATAAGCCCCGACACGTCTCTGCTACTGGAC 1545
                                                                                                                             1546 TGTGGTGAGGGCACGTTTGGGCAGCTGTGCCGTCATTACGGAGACCAGGTGCCT 1605
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                                                                                                                                                                                                                                                                       1606 CTGGGCACCCTGGCTGTGTTTGTGTCCCACCTGCAGGTCACCACACGCAGATCACCACACGG 1660
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .18.2%; Score 145.8; DB 4; Length 2908; 89.1%; Pred. No. 4.1e-34;
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Patent No. 5333403
GENERAL INFORMATION:
APPLICANT: Tavtigian, Sean V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match .18.2%
Best Local Similarity 89.1%
Matches 156; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Pan troglodytes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        , NAME/KEY: CDS
; LOCATION: (1)..(2478)
US-09-564-805-223
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                                                                                398
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APPLICANT: Tavigian, Sean V.
APPLICANT: Tavigian, Sean V.
APPLICANT: Tavigian, Sean V.
APPLICANT: Sinard, Jeaques
APPLICANT: Sommens, Johanna M.
APPLICANT: Sommens, Johanna M.
APPLICANT: Myriad Genetics, Inc.
TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes
TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes
CURRENT APPLICATION NUMBER: US/09/564,805
CURRENT APPLICATION NUMBER: US 60/107,468
PRIOR FILING DATE: 1998-11-06
PRIOR FILING DATE: 1998-11-06
PRIOR FILING DATE: 1999-11-05
NUMBER OF SEQ ID NOS: 240
NUMBER OF SEQ ID NOS: 240
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1596 TGTGGTGAGGGCACATTTGGGCCAGCTGTGCCGTCATTACGGAGACCAGGTGCAGGTC 1655
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    398 TGTGGTGAGGCCACRTTTGGGCAGCTGTGCCGTCATTACGGAGACCAGGTGGACAGGGTC
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Pred. No. 1.1e-32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 145.8; DB 4; Length-
Pred. No. 4.2e-34;
1; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                    ; LOUGATION: (51)...(2531)
; OTHER INFORMATION: coding sequence as in SEQ ID NO:1 US-09-564-805-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Mismatches
| PRIOR APPLICATION NUMBER: US 60/107,468 | PRIOR FILING DATE: 1998-11-06 | PRIOR APPLICATION NUMBER: 09/434,382 | PRIOR FILING DATE: 1999-11-05 | NUMBER OF SEQ ID NOS: 240 | SOGTWARE: Patentin Ver. 2.0 | SEQ ID NO 3 | LENGTH: 2958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 20, Application US/09564805
; Patent No. 6333403
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 89.1%;
Matches 156; Conservative 1
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99.3%;
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LOCATION: (1)...(139)
OTHER INFORMATION: exon 17
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Matches 138; Conservative
                                                                                                                                                                                                                                                                                    FEATURE:
NAME/KEY: misc_feature
LOCATION: (51).(2531)
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                            APPLICANT: Tavingian, Sean V.
APPLICANT: Tavingian, Sean V.
APPLICANT: Tavingian, Sean V.
APPLICANT: Tavingian, Sean V.
APPLICANT: Sinard, Jacques
APPLICANT: Sommens, Johanna M.
APPLICANT: Myriad Genetics, Inc.
TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility
TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes
FILE REFERENCE: 2318-258
CURRENT APPLICATION WUBBER: 108/09/564,805
CURRENT FILING DATE: 2000-05-05
FRIOR APPLICATION NUMBER: 05/0107,468
FRIOR APPLICATION NUMBER: 09/434,382
FRIOR FILING DATE: 1999-11-05
FRIOR APPLICATION UNMER: 09/434,382
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TTACGGAGACCAGGTGGACAGGGTCCTGGGCACCCTGGCTGCTGTTTTGTGTCTCCACCT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     342 GCAGTGACTCTTCCTTCTTCTTCTTCTGCAGCCCCGACACGTCTCTGCTACTGGACTGTG 401
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; Patent No. 5670367
; GENERAL INFORMATION:
; APPLICANT: BORNER, F.
; APPLICANT: SCHEIFLINGER, F.
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
; VUMBER OF SEQUENCES: 5.2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6e-21;
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Pred. No. 6e-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 1800 Diagonal Road, Suite 500 CITY: Alexandria STATE: VA COUNTY: U.SA ZIP: 2213-0299 COMPUTER READABLE FORM:
                                                                                                                                                                                                                    Sequence 221, Application US/09564805 Patent No. 6333403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12.8%;
74.9%;
                                                                                           121 GCACGCAGATCACCACACG 139
                                                                   493 GCACGCAGATCACCACACG 511
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Matches 128; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .. (2466)
                                                                                                                                                                                                                                           Patent No. 6333403
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Pate
SEQ ID NO 221
LENGTH: 2470
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LOCATION: (1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; LOCATION: (1)
US-09-564-805-221
                                                                                                                                                                              RESULT 7
US-09-564-805-221
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590 TICCICCGCTTCCAAACTIGCCCAGAGCTTTTGTTACTCATCTCTGGCTAGGAAATGGTT 649
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              470 GCTGCTGTGTTTGTGTCCCCACCTGCACGCAGATCACCACACGGTGAGTGTTGGGCTGGAC 529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    530 CACAAAGCTGGAGCCTGGAGGAGGCACTGCCACGTTGAGTTGGCCCTTTGGCTGCGTCTT 589
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5.0%; Score 39.8; DB 1; Length 7218; illarity 1.3%; Pred. No. 0.087; Conservative 214; Mismatches 156; Indels 0
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CUBRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence I, Application US/09376728
; Patent No. 6372961
; GENERAL INFORMATION:
APPLICANT: Tarcynski, Mitchell C.
APPLICANT: Tarcynski, Mitchell C.
TITLE OF INVENTION: Hemoglobin Genes and Their Use
FILE REFERENCE: 0873
                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMMU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFRAM: (703)683-4109
TELEEX: 899140
                                                                                                                                                                                      CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
                                                                                                                                                                                                                                                                                      EP 91 114 300.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEX: 899149
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1426 YYYYYYYYGTACCA 1440
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STRANDEDNESS: single
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US-08-232-463-14
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Best Local Similarity
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APPLICANT: Su, Xin-zhaun
APPLICANT: wellems, Thomas E.
TITILE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
TITILE OF INVENTION: AND PLASMODIUM FALCIPARUM BRYTHROCYTE BINDING PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          153 TCAGGGTTCCATGGATACTTCTTTGCTATAAAGAGGATGACACATGTAAAATCACCTTTA 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           93 ATAAACTTTTTTTTTTTTTTTTGAFGCCCAGCCTTTGTGTAAGTCTACTTGAAAGGGTT 152
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APPLICANT: WHITE, Owen R.
APPLICANT: PRASER, Claire M.
APPLICANT: PRASER, Claire M.
APPLICANT: VENTER, Cohn C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
TITLE OF INVENTION: TUBERCULOSIS
FILE REPERENCE: 24366-20007.00
CURRENT APPLICATION UNMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
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                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,826B
                                                                                                                                                                                                                                 STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: WIH121.001CP1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 235-0176
TELEFAX: (619) 235-0176
INFORMATION FOR SEQ ID NO: 13:
                                                                                                                                                                                                                Knobbe Martens Olson & Bear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2, Application US/09103840A Patent No. 6294328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29,655
                             Miller, Louis H.
Peterson, David S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 10-SEP-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: 15TEABLESH, Ned
REGISTRATION NUMBER: 29,6
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TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                              Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 19124 base pair
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy o
                                                                                                                                                             NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
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Matches 78; Conser
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GENERAL INFORMATION:
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US-09-103-840A-2
                                              APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                     COUNTRY:
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APPLICANT: Lynn Doucette-Stamm et al
APPLICANT: Lynn UNCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: BEIDERMIDIS FOR DIAGNOSTICS.AND THERAPEUTICS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-108
PRIOR FILING DATE: 1997-108
PRIOR FILING DATE: 1997-108
RIOR FILING DATE: 1997-108
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Pred. No. 0.034;
0; Mismatches 76;
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Pred. No. 0.2;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
    CURRENT FILING DATE: 1999-08-17

EARLIER APPLICATION NUMBER: US 60/097,242

EARLIER FILING DATE: 1998-08-20

NUMBER OF SEQ ID NOS: 4

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 1

LENGTH: 840
CURRENT APPLICATION NUMBER: US/09/376,728
CURRENT FILING DATE: 1999-08-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1951, Application US/09134001C
Patent No. 6380370
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; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-1951
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; Sequence 13, Application US/08487826B
; Patent No. 593827
; GENERAL INPORMATION:
; APPLICANT: Sim, Kim L.
                                                                                                                                                                                                                                                                                                                                                 4.9%;
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Best Local Similarity 69.4%;
Matches 50; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                 85; Conservative
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                                                                                                                                                                                                                                                     NAME/KEY: CDS
LOCATION: (51)...(623)
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Matches 85; Conserv
                                                                                                                                                                                   TYPE: DNA
ORGANISM: Zea mays
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                                                                                                                               OTHER INFORMATION: CDC 1551
OTHER INFORMATION: "n" bases at various positions throughout the sequence
OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: WHITE, Owen R.
APPLICANT: WHITE, Owen R.
APPLICANT: WHITE, Owen R.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
TITLE OF INVENTION: PUBERCULOSIS
FILE REFERENCE: 24366-20007.00
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 1
LENGTH: 4411529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Db 435375 decrecareceaedecereeceaedreeceeedeceeeaeceeeaerereeaaeceeee 435434
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                                                                                                                                                                                                                                                                                                                                                                                                                                            419 CAGCTGTGCCGTCATTACGGAGACCAGGTGGACAGGGTCCTGGGCACCCTGGCTGCTGTG 478
                                                                                                                                                                                                                                                                                                                                                        359 CTTCTCTTCTGCAGCCCCGACACGTCTCTGCTACTGGACTGTGGTGAGGGCACRTTTGGG 418
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                                                                                                                                                                                                                                                                  Length 4403765;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4.6%; Score 36.6; DB 4; Length 4411529; 50.9%; Pred. No. 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Db 435435 CATGGTCGCCACGAACTCGCCGCACCGGGACTGGCCGG 435479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     80; Indels
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                                                                                                                                                                                                                                                              Score 36.6; DB 4;
Pred. No. 25;
1; Mismatches 80;
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                                                                                   TYPE: DNA ORGANISM: Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1, Application US/09103840A
Patent No. 6294328
                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 50.9%;
Matches 84; Conservative 1
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
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Matches 84; Conservative
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                                                               LENGTH: 4403765
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US-09-103-840A-1
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US-09-103-840A-1
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Sequence 261, Application US/09461697 Patent No. 6277974

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APPLICANT: Borney, Shawn
APPLICANT: Barney, Shawn
APPLICANT: Barney, Shawn
APPLICANT: Do. Donald C.
APPLICANT: Do. Donald C.
APPLICANT: Portbury, Stuart D.
APPLICANT: Portbury, Stuart D.
APPLICANT: Portbury, Stuart D.
APPLICANT: Puranam, Kasturi
APPLICANT: Ratz, Lawrence C.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING
TITLE OF INVENTION: CELL DEATH
FILE REFERENCE: 10001-005-999
CURRENT APPLICATION NUMBER: US/09/461,697
CURRENT FILING DATE: 1999-12-14
NUMBER OF SEQ ID NOS: 466
SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1152 TITITITITITITITATIAATACCACATCAATTIGAAATTITACAGGAACCAAGATTCAAG 1093
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CURRENT APPLICATION NUMBER: US/09/149,476
CURRENT FILING DATE: 1998-09-08
EARLIER FILING DATE: 1998-03-06
EARLIER FILING DATE: 1997-03-07
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APPLICANT: COGENT NEUROSCIENCE, Inc.
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Best Local Similarity 51.9%;
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CRGANISM: Homo sapiens
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US-09-149-476-255/c
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NUMBER: 6 1997-05-	NUMBER: 60/047,5 1997-05-23 NUMBER: 60/047,4 1997-05-23 NUMBER: 60/047,6 1997-05-23 NUMBER: 60/047,5 1997-05-23 NUMBER: 60/047,5 1997-05-23 NUMBER: 60/047,6 1997-05-23 NUMBER: 60/047,6 1997-05-23 NUMBER: 60/047,6 1997-05-23 NUMBER: 60/047,6 1997-05-23 NUMBER: 60/043,5 1997-05-23 NUMBER: 60/043,5 1997-04-11 NUMBER: 60/043,5 1997-04-11 NUMBER: 60/043,5 NUMBER: 60/043,5 NUMBER: 60/043,5 NUMBER: 60/043,5 NUMBER: 60/043,5 NUMBER: 60/043,5	NUMBER: 60/043,311 1997-04-11 NUMBER: 60/043,671 1997-04-11 NUMBER: 60/043,669 1997-04-11 NUMBER: 60/043,312 1997-04-11 NUMBER: 60/043,313 1997-04-11 NUMBER: 60/043,313 1997-04-11 NUMBER: 60/043,313 1997-04-11 NUMBER: 60/043,672 1997-04-11 NUMBER: 60/043,672 1997-04-11 NUMBER: 60/043,672 1997-08-22 NUMBER: 60/056,886 1997-08-22 NUMBER: 60/056,889 11997-08-22 NUMBER: 60/056,893
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4.5%; Score 36; DB 4; Length 2664;
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Search completed: May 17, 2003, 17:27:33 Job time: 2436.07 secs

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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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Tissue Procurement: ATCC
CDNA Library Preparation
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Tissue Procurement: ATCC
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MCC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12140 row: n column: 03
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Location/Qualifiers
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AA811170 0b42c03.s
AI500718 tn94b10.x
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                                                                                                                      May 17, 2003, 15:56:54; Search time 681.842 Seconds (without alignments) 11900.029 Million cell updates/sec
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                                                                                                                                                                  /tissue_type="retinoblastoma"
| Jab host="DH108 (phage-resistant)"
| Jab host="DH108 (phage-resistant)"
| John Charles | Japan | Japan
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I (bases 1 to 345)
III (bases 1
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5502530"
/clone_lib="NIH_MGC_67"
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/organism="Homo sapiens"
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/clone="InAGE:3061957"
/clone="InAGE:3061957"
/clone="type="lymph"
/cell type="germinal center B cells"
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/note: pT713-pac; Site_1: Not1; No
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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Tissue Procurement: Louis M. Staudt, M.D., Ph.D. CDNA Library Preparation: M.B. Soares Lab CDNA Library Arrayed by: M.B. Soares Lab DNA Sequencing By: M.B. Soares Lab Clone distribution: MGC clone distribution information can found through the 1.M.A.G.E. Consortium/LLNL at: www.bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      308 GGTATGGAGCTGTGCCGAGGCTTGGGCTCCCCACATAAGCACTAGTCTATAGATGCCTCTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 303.2; DB 10;
Pred. No. 3.7e-81;
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Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AA811170.1 GI:2880781
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ilarity 99.0%;
Conservative
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AA811170
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Best Local Similarity
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Email: cgapbs-remmail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image.html
Insert Length: 737 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /lab_host="DH10B"
/note="Organ: uterus, Vector: pCMV-SPORT6, Site_1: Sall;
Site_2: Not1; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.85 kb. Life Technologies catalog #:
                                                            Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Homo.
                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (Dases 1 to 372)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="taxon:9606"
/clone="IPAGE:2177179"
/clone=lib="NCI_CGAP_Ut2"
/tissue_type="moderately-differentiated endometrial
adenocarcinoma, 3 pooled tumors"
                                                                                                                                                                                         Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                             Seq primer: -40UP from Gibco
High quality sequence stop: 342.
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                                           Homo sapiens
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Best Local Simi
Matches 305;
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                                         ORGANISM
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                                                                                                                 Sequencing Center information can be
                       M.D., Ph.D., David Allman,
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                                                                    Bonaldo, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Seq

Clone distribution: NCI-CGAP clone distribution inf

found through the I.M.A.G.E. Consortium/LINL at:

www-bio.llnl.gov/bbrp/image/image.html

Insert Length: 885 Std Error: 0.00

Seq primer: -40m13 fwd. ET from Amersham

High quality sequence stop: 377.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 396;
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D., D
Ph.D., Gerald Marti, M.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 60.5%; Score 303; DB 9; Length 39
Best Local Similarity 100.0%; Pred. No. 4.7e-81;
Matches 303; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
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/lab_host="DH108"
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hf45a09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone
IMAGE:2934808 3', mRNA Sequence.
                                                 4; Indels
Score 302.6; DB 9;
Pred. No. 6e-81;
0; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 5
AWS92601/c
LOCUS
DEFINITION
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AI500718.1 GI:4392700

ACCESSION.

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/db xref="taxon:9606"
/clone="INACR:291965"
/clone="INACR:291965"
/clone="INACR:291965"
/clone="INACR:291965"
/lab host=="DH108"
/lab host=="DH108"
/note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Bqual amounts of plasmid DNA from three normalized libraries (fetal lung NbHL19W, testis NHT, and B-cell NCI_CGAP_GCBI) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 297480-302087, 682632-687239, 726408-728711, and 729096-731399. Subtraction by Bento Soares and M. Fatin Bonaldo. " 117 the state of the same and the same and the same shall be seen shall be seen and shall be seen and
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                                                                                                                                   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (Sases 1 to 499)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                     Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortum (info@image.llnl.gov) for further information.
Seq primer: -40UP from Gibco
High quality sequence stop: 470.
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IMAGE: 2911965 3', mRNA sequence.
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AW510825.1 GI:7148903
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                                                                                                                                 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
I (bases 1 to 47)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                    Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: -40UP from Gibco
High quality Sequence stop: 451.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    245 AGGACTGGTGCCTGGCACACGCGGGCCCAGGAGGCTGCCACACACGAAGCAGATGA 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 ACTAATTTCATTTCAAGGCAGTTTTTAAAGAAGTCTTGGAAACAGACGGCGGCACCTTTC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     185 ACTAATTTCATTTCAAGGCAGTTTTTAAAGAAGTCATGGAAACAGACGGCGGCACCTTTC 126
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/organism="Homo sapiens"
/organism="taxon:9606"
/clone="IMAGE:2934808"
/clone lib="Soares_NFL_T_GBC_SI"
/lab_host="DH108"
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Pred. No. 1.6e-80;
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/clone="IndexColl spaces"
/lab.host="Holl 8"
/note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site=1: Not I; Site=2: Eco RI; Equal amounts of plasmid DNA from three normalized
| libraries (fetal lung NbHL19W, testis NHT, and B-cell lorg vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified colNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 297480-302087, 682632-687239, 726408-72871, and 729096-731399. Subtraction by Bento Soares and M. Fatima Bonaldo. "
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

    (bases 1 to 531)

                                                                                                                                                                                                                                            Thumblished (1997)
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -400P from Gibco
High quality sequence stop: 459.
Location/Qualifiers
                                                                                                                                                                                      NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP)
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hf17h05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2932185 3', mRNĀ sequence.

    .531
    /organism="Homo sapiens"
    /db_xref="taxon:9606"

                                                         AW572950.1 GI:7237683
                                                                                                                                                                                                                                  fumor Gene Index
                                                                                                                   Homo sapiens
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                                     ACCESSION
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RESULT 8 BQ181829/c

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                             EST 30-APR-2002
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Contract: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Jose Mercuende
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
POUNA=Yes.
                                                                                                                                                                                       Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. I toases 1 to 693. Not. CGAP http://www.ncbi.nlm.nih.gov/ncicgap. Not. CGAP http://www.ncbi.nlm.nih.gov/ncicgap. National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
692 bp mRNA linear EST 30-APR-:
UI-H-EU0-azv-m-08-0-UI.s1 NCI_CGAP_Car1 Homo sapiens cDNA clone
IMAGE: 5854255 3', mRNA sequence.
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Pred. No. 2.1e-80;
0; Mismatches 1; Indels 0;
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TAG_LIB=UI-H-BU0
TAG_TISSUE=osteoarthritic cartilage
TAG_SEQ=TGATCACGCT"
TAG_NA C 174 g 187 t
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99.7%;
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Best Local Similarity 99.7
Matches 302, Conservative
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RESULT 9 BM977567/C LOCUS

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ACCESSION VERSION KEYWORDS SOURCE

ORGANISM

AUTHORS TITLE

JOURNAL

REFERENCE

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Consolis couple.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP CDNA Library Preparation: Ling
Tissue Procurement: DCTD/DTP CDNA Library Preparation: Ling
Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E.
Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing
project Clone distribution: MGC clone distribution information
be found through the I.M.A.G.E. Consortium/Lubin at:
www-bio.lln.gov/bbrp/image/image/image whtml Base Calling / Quality
Scores: PHRED from University of Washingtion Genome Center.
PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley
Drosophila Genome Project. University of Washingtion Genome Center:
PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley
Drosophila Genome Project. University of Washingtion Genome Center:
pttp://www.genome.washington.edu Polyadenylation: Based upon the
presence of a XhoI site followed by a run of 14 or more T residues
at the beginning of the sequence, this CDNA insert was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AW248468 394 bp mRNA linear EST 07-JAN-2000
282640.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2820640 3',
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bummalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (Dases 1 to 394)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Other ESTs: 2820640.5prime
Contact: Robert Strausberg, Ph.D.
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/db_xref="taxon.9606"
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/clone_lib="NIH_MGC_7"
/tissue_type="small_cell_carcinoma"
/cell_line="MGC3"
  Score 301.4; DB 14
Pred. No. 2.2e-80;
0; Mismatches 1;
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High quality sequence stop: 213.
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Location/Qualifiers
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60.2%;
  Query Match
Best Local Similarity 99.77
Matches 302; Conservative
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//dev stage="Adult"
//lab_host="DH10B (Life Technologies) (TI phage resistant)"
//note="Organ: Lung; Vector: pr713-pac (Pharmacia) with a modified polylinker; Site 1: ECOR I; Site 2: Not I;
//U-CF-ENI is a normalized—CDNA library containing the following tissue(s): primary Lung Cystic Fibrosis Epithelial Cells. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand CDNA synthesis was primed with an oligo-of primer containing a Not I site. Double stranded CDNA was ligated to an ECOR I adaptor, digested with Not I, and cloned directionally into pT773-Pac vector. The oligomiclectide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (d7)18 tail. The sequence tag for this library is CTGCTCAGGT.

TAG_LIBEUI-CF-ENI
TAG_TISSUB=Human Lung Epithelial Cell Lines untreated LPS for the Labera of the colleges.
                                                                                                                                                                                                                                                                                                                      BM977567 112 bp mRNA linear EST 21-MAR-2002 UI-CF-EN1-aef-c-19-0-UI.S1 UI-CF-EN1 Homo sapiens cDNA clone UI-CF-EN1-aef-c-19-0-UI 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2024 University of Iowa Med Labs, Iowa City, IA 52242, USA 19135 4666
Fax: 319 356 4666
Fax: 319 356 7171
Email: paul-mccray@uiowa.edu
Tissue Procurement: Dr. M. J. Welsh, University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens .

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

(Dases 1 to 712)

Bonaldo,M.F., Lennon,G. and Soares,M.B.

Normalization and subtraction: two approaches to facilitate gene
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/clone="Ul-CF-EN1-aef-c-19-0-UI"
/clone_lib="Ul-CF-EN1"
/tissue_type="primary Lung Cystic Fibrosis Epithelial
     241 GGTCTAAGTGTCCGAGACTTAACGAAAATAGTATTTCAGCTGCAATAAAGATTGAGTTTG 300
                                      79 GGTCTAAGTGTCCGAGACTTAACGAAAATAGTATTTCAGCTGCAATAAAGATTGAGTTTG 20
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/organism="Homo sapiens"
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                                                                                                                                                                                                                                                ·.
/lab_host="DH10B (phage-resistant)"
/note="Organ: lung; Vector: pOTPB; Site 1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500Dp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
103 c. 97 g. 114 t.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 527)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Robert Strausberg, Ph.D.
Email: Gapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seg primer: -40ml3 fwd ET from Amersham
High quality sequence stop: 463.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                        180
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                                                                                                                                                                                                              DB 10; Length 394;
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/clone="IMAGE:1696476"
/clone_lib="Soares_pregnant_uterus_NbHPU"
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National Cancer Institute, Cancer Genome Anatomy
                                                                                                                                                                                                         Query Match 59.8%; Score 299.8; DB 10; Best Local Similarity 99.3%; Pred. No. 4.4e-80; Matches 301; Conservative 0; Mismatches 2;
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/lab_host="DH10B"
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AI089646.1 GI:3428705
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Contact: Robert Strausberg, Ph.D.

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CCAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

image.llnl.gov/image/Nrml/iresources.shtml

Seq primer: -40UP from Gibco

High quality sequence stop: 239.
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Euteleostomi;
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National Cancer Institute, Cancer Genome Anatomy Project
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae,
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Unpublished (1997)
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AW511765.1
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410 bp mRNA linear EST 28-AUG-1998 clone IMAGE:1654910 3', mRNA sequence. AI033108
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Evkaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 410)
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
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/clone="IMAGE:1304777"
/clone lib="NCI GAP GCB1"
/tissue_type="germinal center B cell"
/lab_host="DH10B"
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Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
              /organism="Homo sapiens"
/db_xref="taxon:9606"
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Matches 300; Conserv
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Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman,
Ph.D., Gerald Marti, M.D.
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 1277 Std Error: 0.00
Seq primer: --don13 fwd. ET from Amersham
High quality sequence stop: 288.
Location/Qualifiers
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          /clone_lib="NCI_CGAP_Kid8"
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/tissue_type="renal_cell_tumor"
/lab_host="BH10B"
/note="Organ: kidney; Vector: pCMV-SPORT6; Site_1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.2 kb. Life Technologies catalog #:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 318)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
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AA766184.1 GI:2817422
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1 (bases 1 to 374)

Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,M., Wylie, B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., WashU-NCI human EST Project
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0; Mismatches 3; Indels 0;
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High quality sequence stop: 368.
Location/Qualifiers
                                                                           organism="Homo sapiens"
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Tel: 314 286 1800

Fax: 314 286 1810

Email: est@wastson.wustl.edu

This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 3011 Std Brror: 0.00

Seq primer: -41ml3 fwd. ET from Amersham.

Location/Qualifiers
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/cloine="InMAGE:650649"
/cloine="Stratagene NT2 neuronal precursor 937230"
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Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. 1
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Job time : 689.842 secs
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Sequence 9129, App Sequence 415, App Sequence 1733, App Sequence 239, App Sequence 54, App1 Sequence 54, App Sequence 114, App Sequence 2942, App Sequence 2942, App Sequence 602, App Sequence 602, App Sequence 104, App Sequence 105, App Sequence

Sequence 806, Apples Sequence 6, Appli Sequence 9, Appli Sequence 6473, Applequence 6474, Applequence 72, Applesquence 72, Applesquence 7967, Applesquence 7967, Applesquence 2000, Appl

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GENERAL INFORMATION:

APPLICANT: Tavitigian, Sean V.

APPLICANT: Tavitigian, Gena V.

APPLICANT: Tavitigian, Gena V.

APPLICANT: Simard, Jacques

APPLICANT: Simard, Jacques

APPLICANT: Myriad Genetics, Inc.

TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility

TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes

TITLE OF INVENTION NUMBER: US/09/988,626

CURRENT FILING DATE: 2001-11-20

PRIOR APPLICATION NUMBER: 09/564,805

PRIOR APPLICATION NUMBER: US 60/107,468

PRIOR APPLICATION NUMBER: US 60/107,468

PRIOR PILING DATE: 1998-11-06

PRIOR PILING DATE: 1998-11-05

PRIOR PILING DATE: 1998-11-05
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US-10-09-318-95-

US-10-1123-15-77-
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                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 28, Application US/09988626; Publication No. US20030044959A1; GENERAL INFORMATION:
                         NUMBER OF SEQ ID NOS: 240
SOFTWARE: PatentIn Ver. 2.0
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NAME/KEY: misc_feature
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LENGTH: 26664
Sequence 15427, A
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Sequence 2320, Ap
Sequence 2145, Ap
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Sequence 206, App
Sequence 107, App
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Sequence 8591, Ap
                                                                                  May 17, 2003, 17:27:39; Search time 63.5169 Seconds (without alignments) 10174.595 Million cell updates/sec
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           GenCore version 5.1.5
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-988-626-27
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APPLICANT: Tavigian, Sean V.
APPLICANT: Tavigian, Sean V.
APPLICANT: Tavigian, Sean V.
APPLICANT: Tavigian, Jacques
APPLICANT: Rommens, Jacques
APPLICANT: Rommens, Johanna M.
APPLICANT: Myriad Genetics, Inc.
TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility
TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility
TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility
TITLE OF INVENTION: Chromosome 120p-Linked Pratalog and Orthologous Genes
CURRENT APPLICATION NUMBER: US/09/988,687
CURRENT PILING DATE: 2001-11-20
PRIOR FILING DATE: 2000-05-05
PRIOR APPLICATION NUMBER: US 60/107,468
PRIOR FILING DATE: 1998-11-06
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100.0%; Pred. No. 1.7e-160;
ive 0; Mismatches 0;
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US-09-988-687-28
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US-09-988-626-28
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100.0%; Pred. No. 1.7e-160;
tive 0; Mismatches 0;
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PRIOR APPLICATION NUMBER: 09/434,382
PRIOR FILING DATE: 1999-11-05
NUMBER OF SEQ ID NOS: 240
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 28
LENGTH: 26664
TYPE: DNA
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Best Local Similarity 100.0
Matches 501; Conservative
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APPLICANT: Simard, Jacques
APPLICANT: Rommens, Johanna M.
APPLICANT: Rommens, Johanna M.
APPLICANT: Rommens, Johanna M.
APPLICANT: Myriad Genetics, Inc.
TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility
TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes
TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes
TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes
TITLE OF INVENTION UNMERS: US/09/988,687
CURRENT APPLICATION NUMBER: 09564,805
PRIOR PLING DATE: 2000-05-05
PRIOR PLING DATE: 199-11-06
PRIOR APPLICATION NUMBER: US 60/107,468
PRIOR FILING DATE: 1999-11-05
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Sequence 3, Application US/09988626
GENERAL INFORMATION:
APPLICANT: Tavitgian, Sean V.
APPLICANT: Treng, David H.F.
APPLICANT: Semard, Jacques
APPLICANT: Myriad Genetics, Inc.
TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility
TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes
FILE REFERENCE: 2318-258
CURRENT APPLICATION NUMBER: US/09/988,626
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Best Local Similarity 100.0%; Pred. No. 1.8e-93;
Matches 303; Conservative 0; Mismatches 0;
    Tavtigian, Sean V. Teng, David H.F.
                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 240
SOFTWARE: PatentIn Ver. 2.0
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OTHER INFORMATION: exon
NAME/KEY: polyA_signal
LOCATION: (636). (641)
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LOCATION: (1)..(228)
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LENGTH: 655
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US-09-988-626-3
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APPLICANT: Tavtiglan, Sean V.
APPLICANT: Tavtiglan, Sean V.
APPLICANT: Tavtiglan, Sean V.
APPLICANT: Tavtiglan, Jacques
APPLICANT: Simard, Jacques
APPLICANT: Rommens, Jacques
APPLICANT: Myriad Genetics, Inc.
TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility
TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes
TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes
TITLE OF INVENTION: OWNBER: US/09/988,626
CURRENT APPLICATION NUMBER: US/09/988,626
CURRENT PILING DATE: 2001-01-20
PRIOR APPLICATION NUMBER: US/05/05
PRIOR FILING DATE: 1998-11-06
PRIOR FILING DATE: 1998-11-06
PRIOR FILING DATE: 1999-11-05
NUMBER OF SEQ ID NOS: 240
SEQ ID NO 27
LENGTH: 655
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1.8e-93;
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Publication No. US20030045704A1
GENERAL INFORMATION:
                                                                                                                                           Sequence 27, Application US/09988626
Publication No. US20030044959A1
GENERAL INFORMATION:
Db 26644 ATTCGCCAAGTCTTTTTGACA 26664
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LOCATION: (1)...(228)
OTHER INFORMATION: exon 24
NAME/KEY: polyA signal
LOCATION: (636)...(641)
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ORGANISM: Homo sapiens
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US-09-988-687-27
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Tavtigian, Sean V.
APPLICANT: Tavtigian, David H.F.
APPLICANT: Tavtigian, David H.F.
APPLICANT: Summans, Johanna M.
APPLICANT: Rommens, Johanna M.
APPLICANT: Rommens, Johanna M.
APPLICANT: Myriad Genetics, Inc.
TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility
ITILE OF INVENTION: Gene and a Paralog and Orthologous Genes
FILE REFERENCE: 2188-258
CURRENT APPLICATION NUMBER: US/09/988,626
CURRENT APPLICATION NUMBER: US/08/64,805
FRIOR FILING DATE: 1998-11-06
FRIOR PRIOR DATE: 1998-11-06
FRIOR APPLICATION NUMBER: 09/434,382
FRIOR FILING DATE: 1998-11-05
FRIOR APPLICATION NUMBER: 09/434,382
FRIOR FILING DATE: 1999-11-05
SOFTWARE: ParentIn Ver. 2.0
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2896 GGTCTAAGTGTCCGAGAGTTAACGAAAATAGTATTTCAGCTGCAATAAGAATTGAGTTTG 2955
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  ; TYPE: DNA

REAULEM: Homo sapiens

REAULEM: NAME/KEY: misc_feature

LOCATION: (51)..(2531)

GTHER INFORMATION: coding sequence as in SEQ ID NO:1
US-09-988-687-3
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                                                                                                                                                                                                         60.5%; Score 303; DB 9; I
100.0%; Pred. No. 4.3e-93;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 223, Application US/09988626; Publication No. US20030044959A1; GENERAL INFORMATION:
                                                                                                                                                                                                         Query Match
Best Local Similarity 100.0
Matches 303; Conservative
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Best Local Similarity 98.7
Matches 299; Conservative
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ORGANISM: Pan troglodytes
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US-09-988-626-223
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NAME/KEY: CDS
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100.0%; Pred. No. 4.3e-93;
iive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                LOCATION: (51)...(2531)
CTHER INFORMATION: coding sequence as in SEQ ID NO:1
US-09-988-626-3
CURRENT FILING DATE: 2001-11-20
PRIOR APPLICATION NUMBER: 09/564,805
PRIOR FILING DATE: 2000-05-05
PRIOR PILING DATE: 1000-05-05
PRIOR FILING DATE: 1998-11-06
PRIOR PILING DATE: 1998-11-05
PRIOR FILING DATE: 1999-11-05
NUMBER: PESQ ID NOS: 240
SOFTWARE: PATENTIN Ver: 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.
Matches 303; Conservative
                                                                                                                                                                                                                                                                                      TYPE: DNA ORGANISM: Homo sapiens
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LOCATION: (51)..(2531)
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Query Match 50.8
Best Local Similarity 93.4
Matches 283; Conservative
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US-09-988-626-225
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US-09-988-626-225
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Sequence 223, Application No. US20030045704A1

GENERAL INFORMATION:

APPLICANT: Tavitisian. Sean V.

APPLICANT: Tavitisian. Simard, Jacques

APPLICANT: Rommens, Johanna M.

APPLICANT: Myriad Genetics, Inc.

TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes

TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes

TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes

TITLE OF INVENTION: Gene and a Paralog

CURRENT APPLICATION NUMBER: US/09/988,687

CURRENT FILING DATE: 2001-11-20

PRIOR PELING DATE: 1999-11-06

PRIOR FILING DATE: 1999-11-05

PRIOR FILING DATE: 1999-11-05

NUMBER OF SEQ ID NOS: 240

SEQ ID NO 223

LENGTH: 2908

LENGTH: 2908

LENGTH: 2908
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                                                  ACTAATTTCATTTCAAGGCAGTTTTTAAAGAAGTCTTGGAAACAGACGGCGGCACCTTTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA ORGANISM: Pan troglodytes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; LOCATION: (1)..(2478)
US-09-988-687-223
                                                                                                                                                                                                                                                                                                           CAA 2908
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US-09-988-687-223
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APPLICANT: Tavidian, Sean V.
APPLICANT: Simard, Jacques
APPLICANT: Rommens, Johanna M.
APPLICANT: Rommens, Johanna M.
APPLICANT: Myriad Genetics, Inc.
TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility
TITLE OF INVENTION: Chromosome 17p-Linked Prostate
TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes
FILE REFERENCE: 218-258
CURRENT APPLICATION NUMBER: US/09/988,626
CURRENT FILING DATE: 2001-11-20
PRIOR FILING DATE: 1999-11-06
PRIOR PILING DATE: 1999-11-05
PRIOR FILING DATE: 1999-11-05
NUMBER OF SEQ ID NOS: 240
SOFTWARE: Patentin Ver. 2.0
SOFTWARE: Patentin Ver. 2.0
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2786 CTCTAATCCAGCAAAGTGATTCCCTGCACAGAGACAAGCAGAGAAACAAGGATCAGTG
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                                                                        GGTCTAAGTGTCCGAGACTTAACGAAATAGTATTTCAGCTGCAATAAAGATTGAGTTTG
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Pred. No. 1.7e-76;
0; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 225, Application US/09988626; Publication No. US20030044959A1; GENERAL INFORMATION:
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236 CAGTGGGTCTAAGTGTCCGAGACTTAACGAAAATAGTATTTCAGCTGCAATAAAGATTGA 295
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CURRENT FILING DATE: 2001-05-23

PRIOR APPLICATION NUMBER: US 60/180,312

PRIOR FILING DATE: 2000-02-04

PRIOR PILING DATE: 2000-02-06

PRIOR PILING DATE: 2000-08-03

PRIOR PLING DATE: 2000-08-03

PRIOR PLING DATE: 2000-10-04

PRIOR PAPLICATION NUMBER: US 60/236,356

PRIOR PLING DATE: 2000-10-04

PRIOR PILING DATE: 2000-10-04

PRIOR PILING DATE: 2000-10-04

PRIOR PILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00663

PRIOR PILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00663

PRIOR PILING DATE: 2001-01-30

PRIOR PILING DATE: 2000-06-30

PRIOR PILING DATE: 20
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OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.3
OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 0.99
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47.2%; Pred. No. 0.44;
tive 0; Mismatches 114;
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OTHER INFORMATION: MAP TO AC009230.2
OTHER INFORMATION: EXPRESSED IN LUNG,
OTHER INFORMATION: EXPRESSED IN BT474
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Matches 102; Conserv
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APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Hanzel, David K.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
                                                                                                    JAPPLICANT: Tartigian, Sean V.
APPLICANT: Tartigian, Sean V.
APPLICANT: Tartigian, Sean V.
APPLICANT: Tartigian, Jacques
APPLICANT: Sinard, Jacques
APPLICANT: Rommens, Johanna M.
APPLICANT: Rommens, Johanna M.
APPLICANT: Myriad Genetics, Inc.
TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes
TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes
TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes
FILE REFERENCE: 2318-258
CURRENT FILING DATE: 2000-11-20
PRIOR FILING DATE: 2000-05-05
PRIOR FILING DATE: 1999-11-05
PRIOR APPLICATION NUMBER: US 60/107,468
PRIOR FILING DATE: 1999-11-05
PRIOR FILING DATE: 1999-11-05
SEQ ID NO 225
LENGTH: 2892
LENGTH: 2892
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Pred. No. 1.7e-76;
0; Mismatches 4;
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                 Sequence 225, Application US/09988687
Publication No. US20030045704A1
GENERAL INFORMATION:
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ilarity 93.4%;
Conservative
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ORGANISM: Gorilla gorilla
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Matches 283; Conserv
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; LOCATION: (1)
US-09-988-687-225
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Length 480;

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Brown, D.
Chang, H.
Zhu, T.
Han, B.
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US-09-880-107-2145
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                                                                                        APPLICANT: Hauge, Brian M.
APPLICANT: Hauge, Jeremy D.
APPLICANT: Parnell, Laurence D.
APPLICANT: Parsons, Jeremy D.
APPLICANT: Parsons, Jeremy D.
APPLICANT: Wang, Ming Li
TITLE OF INVENTION: Soybean Cyst Nematode Resistance
FILE REFERENCE: 38-10(15810)B
CURRENT APPLICATION NUMBER: US/09/754,853A
CURRENT FILING DATE: 2001-01-05
PRIOR PAPLICATION NUMBER: US 60/174,880
PRIOR PILING DATE: 2000-01-07
NUMBER OF SEQ ID NOS: 1119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 6.4%; Score 32.2; DB 9; Length 513509; Best Local Similarity 66.7%; Pred. No. 69; Matches 46; Conservative 0; Mismatches 23; Indels 0;
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6.4%; Score 32; DB 10; Length 1089;
Best Local Similarity 56.7%; Pred. No. 2.5;
Matches 59; Conservative 0; Mismatches 45; Indels
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Patent No. US20020146721A1

GENERAL INFORMATION:

APPLICANT: Berka, Randy M.

APPLICANT: Clausen, ID Groth

TITLE OF INVENTION: Expression

FILE REFERENCE: 10085.500-US

CURRENT APPLICATION UNMBER: US/09/974,300

CURRENT FILING DATE: 2000-10-05

PRIOR APPLICATION NUMBER: 09/680,598

PRIOR PLING DATE: 2000-10-06

PRIOR PLING DATE: 2000-10-06

PRIOR PLING DATE: 2001-03-27

NUMBER OF SEQ ID NOS: 8481

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 2320

LENGTH: 1089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: CDS
LOCATION: (111805)..(113968),(114684)..(115204)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: (1)...(513509)
OTHER INFORMATION: unsure at all n locations
OTHER INFORMATION: Clone ID: 318013_region_A3
US-09-754-853A-4
                        Sequence 4, Application US/09754853A Publication No. US20030005491A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: DNA
; ORGANISM: Bacillus licheniformis
US-09-974-300-2320
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NAME/KEY: unsure
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US-09-754-853A-4
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270 AGTATTTCAGCTGCAATAAAGATTGAGTTTGCAATTGTGAGTTCTTTTGCTTCCTCCTGC 329

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1422 TTGTAGGCAACTGTTTTGGATTTGTGGGGAATCGAATGTTGAATCCTTACTACAATCAGG 1481
132 TTCAAGGCAGTTTTTAAAGAAGTCTTGGAAACAGACGGCGGCACCTTTCCTCTAATCCAG 191
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APPLICANT: Gooper, Bret
TITLE OF INVENTION: Promoters for regulation of plant expression
FILE REPERBNCE: 1360.001U51
CURRENT APPLICATION NUMBER: US/09/887,576
CURRENT PILING DATE: 2001-06-25
PRIOR APPLICATION NUMBER: US 60/213,848
PRIOR APPLICATION NUMBER: US 60/214,087
PRIOR APPLICATION NUMBER: US 60/214,087
PRIOR APPLICATION NUMBER: US 60/258,692
PRIOR APPLICATION NUMBER: US 60/258,692
PRIOR FILING DATE: 2000-12-29
PRIOR APPLICATION NUMBER: US 60/258,692
PRIOR FILING DATE: 2000-12-29
NUMBER OF SEQ ID NOS: 975
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                            Sequence 2145, Application US/09880107; Sequence 2145, Application US/09880107; Patent No. US20020142981A1
; Patent No. US20020142981A1
; APPLICANT: Horne, Darci T.
; APPLICANT: Scherf, Uwe
; APPLICANT: Scherf, Uwe
; APPLICANT: Gene Logic, Inc.
; TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer:
; TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer:
; TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer:
; TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer:
; TITLE OF INVENTION NUMBER: US 60/211,379
PRIOR FILING DATE: 2000-06-14
; PRIOR FILING DATE: 2000-06-14
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 3950
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NOS: 2145
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US-09-880-107-2145
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Patent No. US20020144047A1
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Best Local Similarity 54.2'
Matches 65; Conservative
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ORGANISM: Homo sapiens
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; LENGTH: 2049
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-887-576-655
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Length 2049	חלים	2
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Score 31.4; DB 10;	Pred. No. 5.7;	,
6.3%; S	56.2%;)
Query Match	Best Local Similarity 56.2%;	100 000

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Search completed: May 18, 2003, 00:39:58 Job time : 384.517 secs

Search completed. May 18, 2003, 00.33.58

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Sequence 225, App
Sequence 1, Appli
Sequence 1, Appli
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Sequence 27, Appl
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(cgn2_6/ptodata/2/ina/5A_COMB.seq:*

(cgn2_6/ptodata/2/ina/5B_COMB.seq:*

(cgn2_6/ptodata/2/ina/6A_COMB.seq:*

(cgn2_6/ptodata/2/ina/6B_COMB.seq:*

(cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*

(cgn2_6/ptodata/2/ina/pcTus_COMB.seq:*
        5.1.5
Compugen Ltd.
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US-09-564-805-27

US-09-564-805-223

US-09-564-805-225

US-08-261-822A-1

US-08-261-822A-1

US-08-261-822A-1

US-08-261-822A-1

US-08-261-822A-1

US-08-261-822A-1

US-08-261-822A-1

US-08-261-822A-1

US-08-343-731-5

US-08-343-731-7

US-08-361-083-181
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US-08-843-530B-17
US-08-961-527-192
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                                                                                             US-09-434-382-28_COPY_26164_26664
                                                                                                                                                           441362 segs, 153338381 residues
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        GenCore version
Copyright (c) 1993 - 2003
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Maximum Match 100%
Listing first 45 summaries
                                          nucleic search, using sw model
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; LOCATION: (636)..(641)
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US-09-564-805-3
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Sequence 27, Application US/09564805

Patent No. 6333403

GENERAL INFORMATION:

APPLICANT: Tartigian, Sean V.

APPLICANT: Tartigian, Sean V.

APPLICANT: Simard, Jacques

APPLICANT: Simard, Jacques

APPLICANT: Myriad Genetics, Inc.

TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility

TITLE OF INVENTION NUMBER: US 60/107,468

PRIOR FILING DATE: 1998-11-06

PRIOR FILING DATE: 1999-11-05

NUMBER OF SEQ ID NOS: 240

SOFTWARE: PatentIn Ver: 2.0
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                                                                                                                                                                                                          26524 ACCTTGGAGAAGGCTCTCTGTGCTGTAGTGTGGCAGCTGCCTGGTACCCGGGTGGCTTGG 26583
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                                                                                                                               26164 GGTATGGAGCTGTGCCGAGGCTTGGGCTCCCACATAAGCACTAGTCTATAGATGCCTCTT 26223
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                                                                        Gaps
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                                                                                                          1 GGTATGGAGCTGTGCCGAGGCTTGGGCTCCCACATAAGCACTAGTCTATAGATGCCTCTT
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                                    100.0%; Score 501; DB 4; Length 26664; 100.0%; Pred. No. 6.1e-160;
                                                                      0; Indels
                                                                        0; Mismatches
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LOCATION: (1)...(228)
OTHER INFORMATION: exon 24
NAME/KEY: polyA_signal
                                                     Best Local Similarity 100.0
Matches 501; Conservative
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US-09-564-805-27
 US-09-564-805-28
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LENGTH: 655
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                                      Query Match
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APPLICANT: Tavitidum:
APPLICANT: Tavitidum:
APPLICANT: Tavitidum:
APPLICANT: Simard, Jacques
APPLICANT: Simard, Jacques
APPLICANT: Simard, Jacques
APPLICANT: Simard, Jacques
APPLICANT: Myriad Genetics, Inc.
TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility
TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes
FILE REFERENCE: 2318-258
CURRENT APPLICATION NUMBER: US/09/564,805
CURRENT APPLICATION NUMBER: US 60/107,468
PRIOR PRILING DATE: 1998-11-06
PRIOR PLILING DATE: 1999-11-06
PRIOR FILING DATE: 1999-11-05
NUMBER OF SEQ ID NOS: 240
SOFTWARE: Patentin Ver. 2.0
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                                                                                                                                                                                                                                                                                                                                                      240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                593 GGTCTAAGTGTCCGAGACTTAACGAAAATAGTATTCAGCTGCAATAAAGATTGAGTTTG 652
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                                                                                                                                                              353 GGTATGGAGCTGTGCGAGGCTTGGGCTCCCACATAAGCACTAGTCTATAGATGCCTCTT 412
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Length 655;
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COTHER INFORMATION: coding sequence as in SEQ ID NO:1
US-09-564-805-3
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Best Local Similarity 100.0%; Pred. No. 5.1e-93;
Matches 303; Conservative 0; Mismatches 0;
Query Match 60.5%; Score 303; DB 4; I
Best Local Similarity 100.0%; Pred. No. 2.1e-93;
Matches 303; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 3, Application US/09564805
Patent No. 6333403
GENERAL INFORMATION:
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ORGANISM: Homo sapiens
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NAME/KEY: misc feature
LOCATION: (51)..(2531)
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##FILICANT: Teng, David H.F.
#PELICANT: Simard, Jacques
#PELICANT: Simard, Jacques
#PELICANT: Simard, Jacques
#PELICANT: Simard, Jacques
#PELICANT: Myriad Genetics, Inc.
#PELICANT: Myriad Genetics, Inc.
#PELICANT: Myriad Genetics, Inc.
#PILE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility
#PILE REFERENCE: 2318-28
#CURRENT APPLICATION NUMBER: US/09/564,805
#CURRENT APPLICATION NUMBER: US 60/107,468
#PRIOR PELING DATE: 1998-11-06
#PRIOR FILING DATE: 1999-11-05
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Patent No. 5650553
BARBAL INFORMATION:
APPLICANT: Ecker, Joseph R. et al.
TITLE OF INVENTION:
TITLE OF INVENTION: and Pathogens
NUMBER OF SEQUENCES: 82
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Pred. No. 1.6e-76;
0; Mismatches 4;
                                                                                                                                                                                                                   Sequence 225, Application US/09564805
Patent No. 6333403
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Teng, David H.F.
Simard, Jacques
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Best Local Similarity 93.4
Matches 283; Conservative
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                                                                                                                                                                                                                                                                                   GENERAL INFORMATION
                                                         CAA 2908
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      303
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; LOCATION: (1)
US-09-564-805-225
                                                                                                                                                                                         US-09-564-805-225
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      CAA
                                                                                                                                                                                                                                                                                                                   APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                    LANT: Tartigian, Sean V.

Tartigian, Sean V.

APPLICANT: Teng, David H.F.

APPLICANT: Simard, Jacques

APPLICANT: Rommens, Johanna M.

APPLICANT: Rommens, Johanna M.

APPLICANT: Rommens, Johanna M.

APPLICANT: Rommens, Johanna M.

TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility

TITLE OF INVENTION OF Chromosome 17p-Linked Prostate Cancer Susceptibility

TITLE OF INVENTION OF Chromosome 17p-Linked Prostate Cancer Susceptibility

FILE REFERENCE: 2318-258

CURRENT FILING DATE: 2000-05-05

PRIOR PELICATION NUMBER: 1998-11-05

PRIOR PELICATION NUMBER: 09/434,382

PRIOR PELICATION NUMBER: 09/434,382

NUMBER OF SEQ ID NOS: 240

SEQ ID NO 223

LENGTH: 2908

TYPE: DNA

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ACTAATTTCATTTCAAGGCAGTTTTTAAAGAAGTCTTGGAAACAGACGGCGGCACCTTTC
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                                                            121 ACTAATTTCATTTCAAGGCAGTTTTTAAAGAAGTCTTGGAAACAGACGGCGGCACCTTTC
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Best Local Similarity
Matches 299; Conserv
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; LOCATION: (1)
US-09-564-805-223
                                                                                                                         2776
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200 TICCCTGCACACCCAGAGACAAGCAGAGTAACAGGATCAGTGGGTCTAAGTGTCCGAGACT 259
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Parent No. 595562
GENERAL INFORMATION:
APPLICANT: Ecker, Joseph
APPLICANT: Alonso, Jose
TITLE OF INVENTION: AND PATHOGENS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSE: Woodcock Washburn Kurtz Mackiewicz & No. 5955652ris STREET: One Liberty Place - 46th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 33.2; DB 5; Length 6042; Pred. No. 0.67; 0; Mismatches 73; Indels 0
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/819,288
FILING DATE:
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INPORMATION:
NAME: Beardell, Lori Y.
REGISTRATION NUMBER: 34,293
REGISTRATION NUMBER: UPN-2949
TELECOMMULCATION INFORMATION:
TELEPHONE: 215-568-2100
TELEPHONE: 215-568-3439
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               320 ITCCTCCTGCTGCTACAGAGCAGGGTC 349
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                                                                08/261,822
                             PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: 08/261,82;
FILING DATE: 0me 17, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Beardell, Lori Y.
REGISTRATION NUMBER: 34,293
TELECOMMUNICATION INFORMATION:
TELEPRAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 6042 base pairs
TYPE: mucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 51.3%;
Matches 77; Conservative (
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MEDIUM TYPE: Floppy disk
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HYPOTHETICAL: N
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PCT-US95-07744A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JS-08-819-288-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             200 TTCCCTGCACACCAGAGACAAGCAGAGTAACAGGATCAGTGGGTCTAAGTGTCCGAGACT 259
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STREET: Woodcock, Washburn, Kurtz, Mackiewicz & No. 5650553ris
STREET: One Liberty Place, 46th floor
CTTY: Philadelphia
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GENERAL INFORMATION:
APPLICANT: Trustees of The University of Pennsylvania
APPLICANT: Trustees of The University of Pennsylvania
TITLE OF INVENTION: and Pathogens
NUMBER OF SEQUENCES:
ROUBERS SECUENCES: 82
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz & Norris
STREET: One Liberty Place, 46th floor
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              73; Indels
                                                                                                                                                          ZIP: 19103

COMPUTER READMALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/07744A
FILING DATE: 15-JUNE-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 6.6%; Score 33.2; DB Best Local Similarity 51.3%; Pred. No. 0.67; Matches 77; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                      CURRENT AFFLICATION DATE:

PELLING DATE: 17-JUN-1994
CLASSIFICATION IS 36
ATTORNEY/AGENT INFORMATION:
NAME: Beardell, Lori Y.
REGISTRATION NUMBER: 34,293
TELEPHONE: (215) 568-3100
TELEPHONE: (215) 568-3100
TELEPHONE: (215) 568-3499
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 6042 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                 CORRESPONDENCE ADDRESS: ADDRESSE: Woodcock,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8
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STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
                                                                                                                                                                                                                         .;
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                                                                                                                                                                                  Length 6172;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: ECKET, Joseph
APPLICANT: ECKET, Joseph
APPLICANT: Alonso, Jose
TITLE OF INVENTION: PLANT GENES FOR SENSITIVITY TO ETHYLENE
TITLE OF INVENTION: AND PATHOGENS
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
APPLICATION NUMBER: US/09/400,348
                                                                                                                                                                                                                 73;
                                                                                                                                                                              Query Match 6.6%; Score 33.2; DB 2; Best Local Similarity 51.3%; Pred. No. 0.68; Matches 77; Conservative 0; Mismatches 73;
                                                                                                                                                                                                                                                                                                                                                                                                                    TICCICCIGCIGCIACAGAGCAGGGIC 349
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Patent No. 6355778
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Beardell, Lori Y.
REGISTRATION NUMBER: 34,293
REFERENCE/DOCKET NUMBER: UPN-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEPHONE: 215-568-310
INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
                                                          TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

HYPOTHETICAL: NO

ANTI-SENSE: NO

US-08-819-288-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
LENGTH: 6172 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
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US-09-400-348-1
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260 TAACGAAAATAGTATTTCAGCTGCAATAAAGATTGAGTTTGCAATTGTGAGTTCTTTTGC 319
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                                                                                                                                     750 TTCCTTGAAGATCTGAATGCGTAGATCATACGGGATCTTTGCATTTTTGTTGCTTTTCGT 809
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  Score 33.2; DB 4; Length 6172;
Pred. No. 0.68;
0; Mismatches 73; Indels 0
                                          73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: 186 Human Secreted proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/149,476
CURRENT TILING DATE: 1998-09-08
EARLIER APPLICATION NUMBER: PCT/US98/04493
EARLIER FILING DATE: 1999-03-06
                                                                                                                                                                                                                                                                           320 TICCICCIGCIGCIGCIACAGAGCAGGGIC 349
                                                                                                                                                                                                                                                                                                        810 TTCTTTTGTTGCTGCTTCATACTAAGATC 899
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FILING DATE: 1997-03-07
APPLICATION NUMBER: 60/040,333
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FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,581
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APPLICATION NUMBER: 60/040,163
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FILING DATE: 1997-05-23
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FILING DATE: 1997-05-23
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FILING DATE: 1997-05-23
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FILING DATE: 1997-05-23
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FILING DATE: 1997-03-07
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APPLICATION NUMBER: 60/040,334
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FILING DATE: 1997-05-23
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Patent No. 6420526
6.6%; & nilarity 51.3%; E Conservative 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILE REFERENCE: PZ002P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
  Query Match
Best Local Similarity
Matches 77; Conserv
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AFFLING DATE: 1997-08-22
APPLICATION NUMBER: 60/056,889 AFFLING DATE: 1997-08-22
APPLICATION NUMBER: 60/056,879
APPLICATION NUMBER: 1997-08-22 APPLICATION NUMBER: 60/047,598 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/047,613 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/047,582 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/047,596 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/047,612 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/047,632 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/047,601 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/043,580 FILING DATE: 1997-04-11 APPLICATION NUMBER: 60/043,314 FILING DATE: 1997-04-11 APPLICATION NUMBER: 60/043,569 FILING DATE: 1997-04-11 FILING DATE: 1997-04-11 APPLICATION NUMBER: 60/043,311 FILING DATE: 1997-04-11 FILING DATE: 1997-04-11 APPLICATION NUMBER: 60/043,312 FILING DATE: 1997-04-11 APPLICATION NUMBER: 60/043,315 FILING DATE: 1997-04-11 FILING DATE: 1997-06-06 APPLICATION NUMBER: 60/056,886 APPLICATION NUMBER: 60/056,893 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,630 APPLICATION NUMBER: 60/056,878 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,637 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,903 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,888 FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/056,880 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,911 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,636 APPLICATION NUMBER: 60/043,568 FILING DATE: 1997-04-11 APPLICATION NUMBER: 60/043,669 APPLICATION NUMBER: 60/043,313 FILING DATE: 1997-04-11 APPLICATION NUMBER: 60/043,672 APPLICATION NUMBER: 60/056,877 APPLICATION NUMBER: 60/056,662 APPLICATION NUMBER: 60/056,882 LICATION NUMBER: 60/043,674 APPLICATION NUMBER: 60/048,974 APPLICATION NUMBER: 60/043,671 FILING DATE: 1997-08-22 1997-08-22 1997-08-22 1997-08-22 1997-08-22 1997-04-11 1997-04-11 1997-04-11 FILING DATE: EARLIER EARLIER EARLIER EARLIER EARLIER EARLIER EARLIER EARLIER EARLIER
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EXPLICATION NUMBER: 60/056,031

R APPLICATION NUMBER: 60/056,631

R FILING DATE: 1997-08-22

R APPLICATION NUMBER: 60/056,845

R FILING DATE: 1997-08-22

R APPLICATION NUMBER: 60/056,892

R APPLICATION NUMBER: 60/057,761

R FILING DATE: 1997-08-22

R APPLICATION NUMBER: 60/057,761

R R PLING DATE: 1997-05-23

R APPLICATION NUMBER: 60/047,595

R FILING DATE: 1997-05-23

R APPLICATION NUMBER: 60/047,595

R FILING DATE: 1997-05-23 EARLIER APPLICATION NUMBER. 5.1 EARLIER FILING DATE: 1997-08-22 EARLIER APPLICATION NUMBER: 60/056,887 EARLIER FILING DATE: 1997-08-22 EARLIER APPLICATION NUMBER: 60/056,908 EARLIER APPLICATION NUMBER: 60/048,964
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/057,650 FILING DATE: 1997-06-13 APPLICATION NUMBER: 60/061,060 FILING DATE: 1997-10-02 APPLICATION NUMBER: 60/056,910 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,864 APPLICATION NUMBER: 60/047,585 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/047,593 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/047,614 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/043,578 FILING DATE: 1997-04-11 APPLICATION NUMBER: 60/056,632 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,881 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,909 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,875 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,884 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/047,586 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/047,590 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/047,594 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/043,576 FILING DATE: 1997-04-11 APPLICATION NUMBER: 60/057,669 APPLICATION NUMBER: 60/049,610 APPLICATION NUMBER: 60/056,874 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/047,589 60/043,670 LICATION NUMBER: 60/056,664 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,876 60/047,501 PPLICATION NUMBER: 60/ ILING DATE: 1997-05-23 ILING DATE: 1997-08-22 1997-09-05 FILING DATE: 1997-05-23 FILING DATE: 1997-05-23 FILING DATE: 1997-04-1 APPLICATION NUMBER: EARLIER I BARLIER EARLIER DEARLIER DEARLIER DEARLIER EARLIER EARLIER EARLIER EARLIER

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13 TGCCGAGGCTTGGGCTCCCACATAAGCACTAGTCTATAGATGCCTCTTAGGACTGGTGCC 72
                                                                                                                                                                                                                                                                                                Squence 11, Application US/09579181

Patent No. 6365372

GENERAL INFORMATION:

APPLICANT: Chrivia, John

APPLICANT: Yaciuk, Peter

TITLE OF INVENTION: SNP2 Related CBP Activator Protein (SRCAP)

FILE REFERENCE: 16153-425

CURRENT APPLICATION NUMBER: US/09/579,181

CURRENT FILING DATE: 2000-05-25

PRIOR APPLICATION NUMBER: 60/136,620

PRIOR APPLICATION NUMBER: 06/136,620

PRIOR PILING DATE: 1999-05-27

NUMBER OF SEQ ID NOS: 17

SOFTWARE: PatentIN Ver: 2.0

SEQ ID NO 11

LENGTH: 8916
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US-09-579-181-10/C

Sequence 10, Application US/09579181.
Fatent No. 365572.
GENERAL INFORMATION:
APPLICANT: Chrivia, John
TITLE OF INVENTION:
FILE REPERENCE: 16153-4247
CURRENT APPLICATION NUMBER: US/09/579,181
CURRENT APPLICATION NUMBER: 60/136,620
FRIOR APPLICATION NUMBER: 60/136,620
FRIOR FILING DATE: 1999-05-27
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PatentIN Ver. 2.0
SEQ ID NO 10
LENGTH: 9354
                                            .
0
  Length 2327;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6.2%; Score 31.2; DB 4; Length 8916; llarity 50.7%; Pred. No. 4; Conservative 0; Mismatches 73; Indels 0
                                          Indels
Query Match 6.2%; Score 31.2; DB 4; I
Best Local Similarity 35.9%; Pred. No. 1.8;
Matches 33; Conservative 28; Mismatches 31;
                                                                                                                                                                                        1636 AAKKSGGCASGAGCCAGAACCTGCATTGCTT 1667
                                                                                                                                                               387 AGTGTGGCAGCTGCTGGTACCCGGGTGGCTT 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6780 ACAGGTTTGGGCTGGAGGCGGTGTATGA 6753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 133 TCAAGGCAGTTTTTAAAGAAGTCTTGGA 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: DNA
; ORGANISM: Human
US-09-579-181-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; ORGANISM: Human
US-09-579-181-10
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DETECTING
TITLE OF INVENTION: ALTERED TYPE I OR TYPE IX COLLAGEN GENE SEQUENCES
NUMBER OF SEQUENCES: 666
                                                                                                                                                                                                                                                                  7278 TGAGGCAGAGATGGGCACAGAAGGTGGACCAAGCAAGAGAGGAGGAGAAGGAGGTTACAAG 7219
                                                                                                                                                                   7338 reccaareceresecacacaereresecreasecercaaseceaaseseasinasisae 7279
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                                                                                                                        13 TGCCGAGGCTTGGGCTCCCACATAAGCACTAGTCTATAGATGCCTCTTAGGACTGGTGCC 72
                                                                        .;
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                           DB 4; Length 9354;
                                                                        Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURSTYTARE: DatentIn Release #1.0, Version #1.30
CLEASIFICATION DATA:
APPLICATION NUMBER: US/08/943,731
FILING DATE: 14-MAR.1997
CLEASIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/212,322
FILING DATE: 14-MAR.1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/803,628
FILING DATE: 03-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: DOYLE LEARY Ph.D., KATHRYN
REGISTRATION NUMBER: 36,377
REGISTRATION NUMBER: 36,377
REGISTRATION NUMBER: 36,377
                      Score 31.2; DE
Pred. No. 4.2;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                  7218 ACAGGTTTGGGCTGGAGGCGGTGTATGA 7191
                                                                                                                                                                                                                                                                                                                133 TCAAGGCAGTTTTTAAAGAAGTCTTGGA 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROCKOP, DARWIN J.
SPOTILA, LORETTA D.
DELITAS, CONSTANTINOS D.
SEREDA, LARISA
LARSON, ANDREA W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 200, Application US/08943731
Patent No. 6265157
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TELEPHONE: 215-965-1284
TELEFAX: 215-567-2991
                      6.2%;
ilarity 50.7%;
Conservative 0
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MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PACK, MICHAEL COLIGE, ALAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 787 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EARLY, JAMES
KORKKO, JARMO
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
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US-08-943-731-200/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
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. IUPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-943-731-5
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CRGANISM: Human
US-09-734-675-3
                                                                                                                                                                                                                                                                                                                                                                                                                                           497 TGACA 501
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     293
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APPLICANT: SEREDA, LARISA
APPLICANT: SEREDA, LARISA
APPLICANT: SEREDA, LARISA
APPLICANT: LARSON, ANDREA W.
APPLICANT: COLIGE, ALAIN
APPLICANT: COLIGE, ALAIN
APPLICANT: COLIGE, ALAIN
APPLICANT: COLIGE, ALAIN
APPLICANT: CORKKO, JARNO
APPLICANT: ALA-KOKKO, LEENA, et al.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DETECTING
TITLE OF INVENTION: ALTERED TYPE I OR TYPE IX COLLAGEN GENE SEQUENCES
NUMBER OF SEQUENCES: 666
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                   280 TGGGGGGCCCACTCTGCCCAGTGGTGCTACCCACCCACTCTTCCCGTGTCCTCT 221
                                                                                                                                                                              377 TCTGTGCTGTAGTGTGGCAGCTGCCTGGTACCCGGGTGGCTTGGAAGAAGTCAGCTCCCG 436
                                                                                                                                                                                                                       340 TCTGGGCTGAGGCTGGGCACCCAGGAAGGAAGGAAGGTCCCGCACGGGTGCCCGGGACCC 281
                                                                                                                                                                                                                                                                                   437 TCGTAGTGAGCACCTCTGGAACCTGTCCTCAGAGAGCCACCCTTATTCGCCAAGTCTTTT 496
                                                                                                                                Gaps
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                                                                    6.1%; Score 30.6; DB 4; Length 787; 52.8%; Pred. No. 1.6; tive 0; Mismatches 59; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPTAY: USA
CONTRY: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPTUTER: IBM PC compatible
COMPATE: DatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/943,731
FILING DATE: 03-OCT-1997
CLASSIFICATION: DATA:
APPLICATION NUMBER: US 08/212,322
FILING DATE: 14-MAR.1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/803,628
FILING DATE: 03-DEC-1991
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 36,317
REGISTRATION NUMBER: 36,317
REGISTRATION NUMBER: 36,317
RELECOMMULICATION NUMBER: 36,317
RELECOMMULICATION INFORMATION:
TELECOMMULICATION INFORMATION:
TELECOMMULICATION INFORMATION:
TELEFRENCE/DOCKET NUMBER: 36,317
RELECOMMULICATION INFORMATION:
TELEFRENCE/DOCKET NUMBER: 36,317
RELEFRENCE/DOCKET NUMBER: 35,317
TELEFRENCE/DOCKET NUMBER: 35,317
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US-08-943-731-5/c
; Sequence 5, Application US/08943731
; Patent No. 6265157
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROCKOP, DARWIN J.
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INFORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS: LENGTH: 20084 base pairs TYPE: nucleic acid stranbedness: single
                                                                                                                             66; Conservative
                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                          497 TGACA 501
                                                                                                                                                                                                                                                                                                                                                                                                                                              220 GTGCA 216
                     US-08-943-731-200
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GENERAL INFORMATION:
APPLICANT: WEBSTER, Marion et al
APPLICANT: WEBSTER, Marion et al
APPLICANT: WEBSTER, Marion et al
TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,
TITLE OF INVENTION: USES THEREOF,
CURRENT APPLICATION NUMBER: US/09/734,675
CURRENT FILING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FASTSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                 Db 14248 TGGGAGTGCCCACCTCTGCCCAGTGGTGCTACCCACCCTTACTTCCCGTGTCCTCT 14189
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Db 31519 ATTCCTGCCTATGTGAGAAGGTTATTCCTAGTTCCTTAATGGTAGACTGAGAATCAA 31460
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                                                                                                                                                       377 TCTGTGCTGTAGTGTGGCGGCTGCCTGGTACCCGGGTGGCTTGGAAGAAGTCAGCTCCCG 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               437 TCGTAGTGAGCACCTCTGGAACCTGTCCTCAGAGAGCCACCCTTATTCGCCAAGTCTTTT 496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           113 GCAGATGAACTAATTTCATTTCAAGGCAGTTTTTAAAGAAGTCTTGGAAACAGACGGCGG 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               233 GATCAGTGGGTCTAAGTGTCCGAGACTTAACGAAAATAGTATTTCAGCTGCAATAAAGAT
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Length 20084;
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Best Local Similarity 46.5%; Pred. No. 15;
Matches 99; Conservative 0; Mismatches 114; Indels
                                                                             Indels
Query Match
6.1%; Score 30.6; DB 4; 1
Best Local Similarity 52.8%; Pred. No. 10;
Matches 66; Conservative 0; Mismatches 59;
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Job time : 72.1908 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 15
US-09-734-675-3/c
; Sequence 3, Application US/09734675
; Patent No. 6365391
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May 17, 2003, 15:56:54; Search time 1298.06 Seconds (without alignments) 11232.524 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                           1 ggtatggagctgtgccgagg......tcgccaagtcttttgaca 501
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GenCore version 5.1.5
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             2054640 seqs, 14551402878 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                     US-09-434-382-28_COPY_26164_26664
501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                         OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                              IDENTITY NUC
Gapop 10.0 , Gapext 1.0
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gb ba: *
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em pa: *
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Maximum DB seq length: 2000000000
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

uo	Ношо	HOMO B	Homo	номо в Рап tr	Sequen	HOMO S	Homo sapi	Gorill	Sequence	Seguen	AX326672 Sequence	Seguen	Ratt	AF348157 Mus muscu	Ношо	X72204 Balaenopter	ACOS8799 Homo sapi	AC097359 Homo sapi	Ar429315 Homo sapi AC087159 Mus muscu	AL133305 Human chr	AC013529 Homo sapi	AC010347 HOMO SAPI AC026992 Homo sapi	AC004830 Homo sapi	AL/31655 Mus muscu AC105707 Rattus no	Rattus	Rattu	Rattus	Mus mus Homo sa	Homo sa	Homo sa	AC117334 Rattus no			DNA linear PRI 23-JUL-1998 PRPK 597 M 12 COMPLETE SECTIONS				aniata; Vertebrata; Euteleostomi; tarrhini; Hominidae; Homo.	Nusbaum, C. and Lander, E. e. hRPK.597 M 12	1
	0 %	AK074244 BC001939	BC004158	AKU94687 AF308698	AX405825	AK094333 AK094012	AK001392	G60268 AF308694	AX069570	G42927 AX326639	AX326672	AX326638 AX326659	AC097911	AF348157	AF429315	MIBMCG	AC058799	AC097359	AF429315 AC087159	CNS01DUO	AC013529	AC026992	AC004830	AL731655 AC105707	AC111963	AC126180	AC126082	AC104653	AC069268	AC069399	AC117334	ALIGNMENTS		118788 bp				Chordata; Cran Primates; Cata	inton, L., 17. clone	
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Score	30.	О С	301.4	שפע	· σ (שפ	000	ດ α	•	133.4	95.4	20 C	48.2	42.7	41.4	40.2	9.60	9 6 6	37.8	36.8	36.8	36.6	36.4	3.0 4.0 4.0	35.6	35.4	35.4	35.4	35.2	35.2	35.2			2						
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complement (11824, .11884)
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ement (1000)
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complement (21071. .21100)
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complement(11928
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            Birren, B., Fasman, K., Linton, L., Nusbaum, C., Lander, E., Allen, N., Barker, J., Baldwin, J., Barna, N., Beckerly, R., Benn, J., Boatin, C., Boute, J., Brown, A., Castle, A., Cerry, J., Cooke, P., Depayre, E., Devon, K., Dewar, K., Donelan, L., Etemadi, S., Ferreira, P., FitzHugh, W., Forrest, C., Funke, R., Gage, D., Gardyna, S., Genshelmer, S., Geraglery, K., Gilmartin, T., Grant, G., Hagos, B., Harris, K., Horton, L., Howland, J.C., Hui, L., Jacotoc, L., Kann, L., Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., Meldrim, J., Mohla, M., Morris, W., Morrow, J., Mychaleckyj, J., Nahf, R., Naylor, J., Niloff, M., O'Connor, T., Pavlin, B., Peterson, K., Riley, R., Roberts, D., Rossello, R., Roy, A., Stange-Thomann, N., Stilwell, J., Stojanovic, N., Stone, C., Strickland, C., Subramanian, A., Torruella Miller, I., Vassiliev, H., Vo, A., Wagner, A., Wang, B., Wheeler, J., Wu, Y., Ye, W.J., Zhao, J. and
                                                                                                                                                                                                                                                                                                                            Direct Submission

Submitted (10-JUL-1998) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

(Bases 1 to 118788)

Birren,B., Fasman,K., Linton,L., Nusbaum,C., Lander,E., Allen,N., Barten,J., Barna,N., Beckerly,R., Benn,J., Boatin,C., Botwell,C., Brown,A., Castle,A., Cerny,J., Cooke,P., Depayre,E., Devon,K., Dewar,K., Donelan,L., Etemadi,S., Ferreira,P., FitzHugh,W., Forrest,C., Funke,R., Garge,D., Gardyna,S., Genshelmer,S., Geraglery,R., Gilmartin,T., Garatt,G., Hagos,B., Harris,K., Horton,L., Howland,J.C., Hui,L., Jacotot,L., Maduad,J.C., Hui,L., Jacotot,L., Manguis,N., McEwan,P., McGurk,A., McKernan,K., Meldrim,J., Molla,M., Morris,W., Morrow,J., MyChaleckyj,J., Nabl,R., Naylor,J., Niloff,M., O'Connor,T., Paviln,B., Peterson,K., Riley,R., Roberts,D., Rossello,R., Roy,A., Shyam,R., Strickland,C., Subramanian,A., Torruella-Miller,I., Vas,A., Cando,J. and Zody,M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (23-JUL-1998) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA 0. Ull 1998 this sequence version replaced gi:3335015. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Only the first 118.8 kilobases of this clone are being submitted. The remainder overlaps accession number AC005274 (WICGR project L350).
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clone lib="RPCI-11 human BAC library"
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi, Bukaryota, Metazoa, Chordata, Catarrhini, Hominidae, Homo.

(basea 1 to 2908)

Tavtigian, S.V., Simard, J., Teng, D.H.F., Abtin, V., Baumgard, M., Beck, A., Camp, N.J., Carillo, A.R., Chen, Y., Dayananth, P., Carillo, A.R., Chen, Y., Dayananth, P., Chan, Y., Dayananth, P., Chaffari, S., Gupte, J.S., Hu, R., Tilev, D., Janecki, T., Kort, E.N., Laivy, K.E., Leavitt, A., Leblanc, G., McArthur-Morrison, J., Pederson, A., Penn, B., Peterson, K.T., Reid, J.E., Richards, S., Schroeder, M., Smith, R., Snyder, S.C., Swedlund, B., Swensen, J., Thomas, A., Tranchant, M., Woodland, A.M., Labrie, F., Skolnick, M.H., Neubussen, S., Rommens, J. and Cannon-Albright, L.A.

A candidate prostate cancer susceptibility gene at chromosome 17p. Nat., Genet. 27 (2), 172-180 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
Submitted (12-SEP-2000) Myriad Genetics, Inc., 320 Wakara Way, Salt
Lake City, UT 84108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /translation="MWALCSLLRSAAGRTMSQGRTISQAPARRERPRKDPLRHLRTRE
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DTSLLLDCGEGTFGQLCRHYGDQVDRVLGTLAAVFVSHLHADHHTGLPSILLQRERAL
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HPDIFPLLTSFRCKKEGPTLSVPMVQGECLLKYQLRPRREWQRDAIITCNPEEFIVEA
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ISSLLRTCDLEEFQTCLVRHCKHAFGCALVHTSGWKVVYSGDTMPCEALVRMGKDATL
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/product="putative prostate cancer susceptibility protein
HPC2/ELAC2"
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Tavtigian, S.V., Simard, J., Teng, D. H.F., Baumgard, M., Beck, A.,
Tavtigian, S.V., Carillo, A.R., Chen, Y., Dayananth, P., Desrochers, M.,
Dumont, M., Farnham, J.M., Frank, D., Frye, C., Ghaffari, S.,
Gupte, J.S., Hu, R., Iliev, D., Janecki, T., Kort, B.N., Laity, K.E.,
Leavitt, A., Leblanc, G., McArthur-Morrison, J., Pederson, A., Penn, B.,
Sryder, S.C., Sedlund, B., Skensen, J., Thomas, A., Tranchant, M.,
Woodland, A.-M., Labzie, F., Skolnick, M.H., Neuhausen, S., Rommens, J.
                                                   Db 104236 AAGAAGTCAGCTCCCGTCGTAGTGAGCACCTCTGGAACCTGTCCTCAGAGAGCCACCCTT 104295
                                                                                                                                                                                                                                                                                                        Homo sapiens putative prostate cancer susceptibility protein
HPC2/ELAC2 mRNA, complete cds.
                             AAGAAGTCAGCTCCCGTCGTAGTGAGCACCTCTGGAACCTGTCCTCAGAGAGCCACCCTT
                                                                                                                                                                                                                                                                                         linear
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'db_xref="GI:10880933"
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="17"
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1. .2481
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llarity 100.0%; Pred. No. 5.9e-161;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                            note="Single-stranded coverage."
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complement(56912..26990)
/rpt_family="MER21B"
26991..27290
/rpt_family="Alusx"
complement(27291..27975)
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28034...28197
/rpt_family="LTR28"
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/rpt family="purine-rich"
complement (26122. .26291)
/rpt family="MLTID"
26312. .26337
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/rpt_family="L2"
complement(25697. .25985)
/rpt_family="MLTID"
25816. .25895
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complement(26576. .2678
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28843. .2801
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28920. .29005
                        family="AluSx"
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                                                                     rpt_family="L1M4"
1799. .22104
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rpt_family="MSTA"
3978. .24287
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29140. .29233
  complement (21101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens cDNA FLJ23664 fis, clone HEP03495, highly similar to Putative prostate cancer susceptibility protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NEDO human cDNA sequencing project supported by Ministry of Gronomy, Trade and Industry of Japan; CDNA full insert sequencing; Research Association for Biotechnology; CDNA full insert sequencing, 5'- & 3'-end one pass sequencing: Departent of Virology and Human Genome Center, Institute of Medical Science, University of Tokyo (partly supported by Science and Technology Agency).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kawabata, A., Hikiji, T., Kobatake, N., Inagaki, H., Ikema, Y., Okamoto, S., Okitani, R., Ota, T., Suzuki, Y., Obayashi, M., Nishi, T., Shibahara, T., Tanaka, T., Nakamura, Y., Isogai, T. and Sugano, S. NEDO human cDNA sequencing project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       oligo capping; fis (full insert sequence).
Homo sapiens hepatoma cell_line:HepG2 cDNA to mRNA, clone_lib:HEP
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Direct Submission
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                                                                                                                  Length 2908;
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                                                                                                                  60.5%; Score 303; DB 9;
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                                                                                                                                  Best Local Similarity 100.
Matches 303; Conservative
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/organism="Homo sapiens" /db_xref="taxon:9606"

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Submitted (29-030-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae,
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clone MGC:4102 IMAGE:2820640, mRNA, complete cds.
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/clone="HEP03495"
/cell_line="HepG2"
/cell_type="hepatoma"
/clone_lib="HEP"
/note="cloning vector: pl
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
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                  Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov Series: IRAL Plate: 9 Row: i Column: 17 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 7022621. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                         /trānslation="MWALCSLLRSAAGRTWSQGRTISQAPARRERPRKDPLRHLRTRE
RRPSGSCGGROFNTYLOVHAGSRDSCAALVYBESPRNYLTHCGEGVGRWGEHKLKV
ARLDNIFLTRHWWSWUGGLSGMILTLKETGLRCVLSGPPQLEKYLBAIKIFGSFUKG
IELAVRPHSAPEYEDETMTVYQIPIHSEQRRGKHQPWGSPERPLSRLSPERSSDSELN
BENPHLLPRGVSQRRGYRDSSLVVAFICKLHLKRGMFLVLKARMGLPVGTAALAPITA
AVKDGKSITHEGREILAELCTPPPDPQAARTVVVECPDRSFIQPICGRATTGRYGKYGKAD
APVALVVHMAPASVLVDSRYQQWMERFGPDTQHLVLNENCASVHNLRSHKIGTGLNII
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LQLPNFQQSVQEYRRSAQDGPAPAEKRSQYPEI I FLGTGSA I PMKI RNVSATLVNI SP
DTSLLLDCGEGTFGQLCRHYGDQVDRVLGTLAAVFVSHLHADHHTGLPSILLQRERAL
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ISSLLRTCDLEEFQTCLVRHCKHAFGCALVHTSGWKVVYSGDTWPCEALVRMGKDATL
LIHEATLEDGLEEEAVEKTHSTTSQAISVGMRMNAEFIMLNFSQRYAKVPLFSPNFS
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                                                                                                                                                                                                                                                                                                                                                                      /codon_start=1
/produc="putative prostate cancer susceptibility protein"
/protein_id="AAH01939.1"
/db_xref="GI:12804973"
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/db_xref="LocusID:60528"
/db_xref="Laxon:9606"
/dlone="MGC:4102 IMAGE:2820640"
/tissue type="Lung small cell carcinoma"
/lab_host="NHH MGC_7"
/note="NUCTOR: pOTB7"
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Pred. No. 2.6e-92;
0; Mismatches 1;
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PRI 12-JUL-2001

BC004158 3006 bp mRNA linear PRI 12-JUL Homo sapiens, putative prostate cancer susceptibility protein, clone MGC:2441 IMAGE:2820640, mRNA, complete cds.

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/translation="MWALCSLLRSAAGRTWSQGRTISQAPARERPRKDPLRHLRTRE
KREPSGCGGORDTVILOVAGSRDSCAALVYBERRNILKNGGGOVDLMOGHKLKV
KREPSGCGGORDTVILOVAGSRDSCAALVYBERRNILKNGGGOVDLMOGHKLKV
KREPSGCGGORDTVILOVAGSAALVYBERRNILTRKGGGOVDLMOGHKLKV
IELAVRPHSAPEYEDETWITVYQIPITHSEQRRGKHQPWOSPERPLSRLSPERSEDSELN
RNUBPHLLPHGVSQRRGYRDSSLVVAFTCKHLKKRGMEPVTAKRKGLPVTATATAPIN
AVKDGKSITHEGRELLLAEELCTPPDPGGARVVVCEDDESTIQPICTATATAPINA
APVALVVHMAPASVLVDSRYQQMMERPGPDTQHLVLNENCASVHNLRSHKIQTQLNLI
HDDIPPLITSRRCKKGGPTLSVPWYQGGCLLKYCRPREWQRNJITTGVBREFTURA
LQLPNFQOSVQEYRSAQDGGAPAEKRSQYPBITELGGSATPPMINNISHILVNISP
TYCLLPROGSVGGGGGGGGCRAYGODGVDRVLGTLAAVFVSHLHADHHTGLPSILLONERAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAL Plate: 2 Row: c Column: 13
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 7022621.

Location/Qualifiers
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EKVGVAFDHMKVCFGDFPTMPKLIPPLKALFAGDIEEMEERREKRELRQVRAALLSRE
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/Ocdon_start=1

/product_iputative prostate cancer susceptibility protein"

/protein_id="MAH04158.1"

/db_xref="GI:13278771"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          contact: amadan@systemsĎiology.org
Anup Madan, Rachel Dickhoff, Jessica Fahey, Stephanie Ford, Julia
Greene, Mark Ketteman and Anuradha Madan
                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

    (bases 1 to 3006)

                                                                                                                                                                                                                                            Submitted (01-MAR-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2675 GGTATGGAGCTGTGCCGAGGCTTGGGCTCCCACATAAGCACTAGTCTATAGATGCCTCTT 2734
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CDNA Library Preparation: Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Institute for Systems Biology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue type="Lung, small cell carcinoma"
/clone lib="NIH MGC_7"
/lab host="DH10B-R"
                                                                                                                                                                                                                                                                                                                                                                                 NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Contal: cgapbs.r@mail.nih.gov
Tissue Procurement: DCTD/DTP
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99.7%; Pred. No. 2.6e
iive 0; Mismatches
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/db_xref="LocusID:60528"
/db_xref="taxon:9606"
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                                 Homo sapiens
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Submitted (04-JUL-2007) Takao Isogai, FLJ Project (HRI Team); 2-6-7
Direct Submission

L Submitted (04-JUL-2002) Takao Isogai, FLJ Project (HRI Team); 2-6-7
Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan

(E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)

NEDO human cDNA sequencing project supported by Ministry of
Economy, Trade and Industry of Japan; DNA full insert sequencing:
Research Association for Biotechnology (RAB); cDNA library
construction: Helix Research Institute (HRI) (supported by Japan
Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB,
HRI, and Biotechnology Center, National Institute of Technology and
Evaluation; clone selection for full insert sequencing: HRI and
RAB; annotation: HRI and RAB.
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2907 bp mRNA linear PRI 15-JUL-2002
Homo sapiens CDNA FLJ37368 fis, clone BRAMY2024530, highly similar
to Homo sapiens prostate cancer susceptibility protein HPC2/ELAC2
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                     2855 CTCTAATCCAGCAAAGTGATTCCCTGCACACCAGAGACAAGCAGAGTAACAGGATCAGTG
                                                          121 ACTAATTTCATTTCAAGGCAGTTTTTAAAGAAGTCTTGGAAACAGACGGCGGCACCTTTC
                                                                                                                                         CTCTAATCCAGCAAAGTGATTCCCTGCACACAGGAGAAGCAGAGTAACAGGATCAGTG
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Homo sapiens amygdala cDNA to mRNA, clone_lib:BRAMY2
clone:BRAMY2024530.
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/clone_lib="BRAMY2"
/note="cloning vector: pME18SFL3"
788 c 839 g 584 t
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Pred. No. 1.3e-91;
0; Mismatches 1;
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/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                              2907 bp
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AK094687.1 GI:21753794
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Best Local Similarity 99.7%;
Matches 300; Conservative
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ORIGIN
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Pan.

1 (Dasses 1 to 2908)
Ear (Dasses)
Tavigian, S.V., Simard, J., Teng, D.H.F., Abtin, V., Baumgard, M.,
Beck, A., Camp, N.J., Carillo, A.R., Chen, Y., Dayananth, P.,
Desrochers, M., Dumont, M., Franham, J. M., Frank, D., Frye, C.,
Ghaffari, S., Gupte, J.S., Hu, R., Iliev, D., Janecki, T., Kort, E.N.,
Laity, K.E., Leavitt, A., Leblanc, G., McArthur-Morrison, J.,
Pederson, A., Penn, B., Peterson, K.T., Reid, J.E., Richards, S.,
Thomas, A., Tranchant, M., Woodland, A.M., Labrie, E., Skolnick, M.H.,
Neuhausen, S., Rommens, J. and Gannon-Albright, L.A.
A candidate prostate cancer susceptibility gene at chromosome 17p
Ellosson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Javigian, S.V., Simard, J., Teng, D.H.F., Baumgard, M., Dayananth, P., Desrochers, M., Dumont, M., Farnham, J.M., Frank, D., Frye, C., Ghaffari, S., Gupte, J.S., Hu, R., Iliev, D., Janecki, T., Kort, E.N., Laity, K., Leavitt, A., Leblanc, G., McArthur-Morrison, J., Schroeder, M., Penn, B., Peterson, R.T., Reid, J.E., Richards, S., Schroeder, M., Smith, R., Snyder, S.C., Swedlund, B., Swensen, J., Tranchant, M., Woodland, A.-M., Labrie, F., Skolnick, M.H., Neubausen, S., Rommens, J. and Cannon-Albright, L.A. Bolitet Submission Submission Myriad Genetics, Inc., 320 Wakara Way, Salt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRI 27-FEB-2001
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2607 GGTATGGAGCTGTGGCCGAGGCTTGGGCTCCCACATAAGCACTAGTCTATAGATGCCTCTT
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Novel nucleic acids and polypeptides
Patent: WO 0222660-A 240 21-MAR-2002;
                                                                                                                                                                                                                                                  /translation="mwalcsllrsaagrtmsqgrtisqaparrerrkdplrhirtre
Krgpsgcsggpntvylqvvaagsrdsgaalyvpsefnrylpncgegigrlmqehkikv
                                                                                                                                                                                                                                                                                                      ARLDNI FLTRMHWSNVGGLSGMILTLKETGLPKCVLSGPPQLEKYLEAIKI FSGPLKG
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Sequence 240 from Patent W00222660.
AX405825
AX405825.1 GI:21439089
                                                                                                                                                                                                /protein_id="AAG24920.1"
/db_xref="G1:10946497"
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....2481
                          Location/Qualifiers
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product="ELAC2"
UT 84103,
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ASLGKPLHPLLVVAPNQLKAWLQQYHNQCQBVLHISMIPAKCLQEGAEISSPAVERL
ISSLLRYCDLEEFQTCLVRHYGHAPCGALVHTSGWKVYSGDTMPCFBLLVRMGKDATL
LIHEATLEDGLEEFQYPSTHISTTSQAISVGRRNNAEFIMLNHFSQRYAKVPLFSPNFS
EKVGVAFDHMKVCFGDFPTMPKLIPPLKALFAGDIEEMEERREKRELRQVRAALLSRE
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KRGPSGCSGGPNTVYLQVVAAGSRDSGAALYVFSEFNRYLFNCGEGVQRLMQEHKLKV
ARLDNIFLTRMHWSNVGGLSGMILTLKETGLPKCVLSGPPQLEKYLEAIKIFSGPLKG
                                                                                                                                                                                                                                                                                                                                                                                                                             IELAVRPHSAPEYEDETMTVYQIPIHSEQRRGKHQPWQSPERPLSRLSPERSSDSESN
BEPBHLPHGYGGRRGVRDSSLVVAFTCKLHLKRGNFUVLKAKEMGLPVGTAA.ABIIA
AVKDGKSITHEGREILAELCTPPDPGAAFVVVCEDDESFIQPICENATPGRYGGKAD
APVALVVHMARASAULVDSRYQGWRRFGPDTQHLVLNENCASVHNLRSHKIGTCLNIL
HPDIFPLLTSFRCKKEGPTLSVPMVQCECLLKYQLRPRREWQRDAIITCNPEEFIVEA
LQLPNFQQSVQEYRRSAQDGPAPAEKRSQYPEIIFLGTGSAIPMKIRNVSATLVNISP
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Homo sapiens cerebellum cDNA to mRNA, clone_lib:BRACE2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               59.2%; Score 296.6; DB 6;
llarity 98.7%; Pred. No. 1.2e-90;
Conservative 0; Mismatches 4;
                                                                                                                                                                            /note="unnamed protein product"
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                                                                                                                                                                                                              /codon_start=1
/protein_id="CAD34932.1"
/db_xref="G1:21439090"
                              1. .2992
/organism="Homo sapiens"
                                                                                                 db_xref="taxon:9606"
Location/Qualifiers
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Homo sapiens
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ACCESSION
    ORGANISM
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ORIGIN
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AK001392
LOCUS
                                                                                                                                                                                                                                         TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                      TITLE
                                                                                AUTHORS
                                                            REFERENCE
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                                                                                                                                                                                                                 Submitted (04-JUL-2002) Takao Isogai, FLJ Project (HRI Team); 2-6-7 Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986) Whord to the configuration of the configuration of the configuration of the configuration for Biotechnology (RAB); cDNA full insert sequencing: Research Association for Biotechnology (RAB) is cupan library of construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: HRI and RAB; annotation: HRI and RAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AK094012 2793 bp mRNA linear PRI 15-JUL-2002 Homo sapiens CDNA FLJ36693 fis, clone UTBRU2008901, highly similar Lo Homo sapiens putative prostate cancer susceptibility protein HPC2/ELAC2 mRNA.
Sugiyama, T., Irie, R., Otsuki, T., Sato, H., Wakamatsu, A., Ishii, S., Mamanoto, J., Isono, Y., Kawai, Hio, Y., Saito, K., Wahishkawa, T., Kimura, K., Yamashita, H., Matsuo, K., Nakamura, Y., Sekine, M., Kikuchi, H., Kanda, K., Wagatsuma, M., Murakawa, K., Kanehori, K., Sudahashi-Teyjii, A., Oshima, A., Sudiyama, A., Kawakami, B., Suzuki, Y., Sugano, S., Naqahari, K., Masuho, Y., Nagai, K. and Isogai, T.
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Homo sapiens uterus cDNA to mRNA, clone_lib:UTERU2
clone:UTERU2008901.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue_type="cerebellum"
/clone_lib="BRACE2"
/note="cloning vector: pME18SFL3"
708 c 724 g 631 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 294.6; DB 9;
Pred. No. 5.7e-90;
0; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="taxon:9606"
/clone="BRACE2010203"
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1. .2734
                                                                                                                                                             2 (bases 1 to 2734)
Isogai,T. and Yamamoto,J.
Direct Submission
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Matches 297; Conservative
                                                                                                                                          Unpublished
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ORIGIN
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DEFINITION
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VERSION
KEYWORDS
SOURCE
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                                                                                                                        TITLE
JOURNAL
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                                                                                                                                                                                                                       JOURNAL
                                                                                                                                                             REFERENCE
                                                                                                                                                                               AUTHORS
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Submitted (04-JUL-2002) Takao Isogai, FLJ Project (HRI Team); 2-6-7 Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan (Famali:genomise@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986) McDO human CDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; CDNA full insert sequencing: Research Association for Biotechnology (RAB); CDNA full insert sequencing: Construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: HRI and RAB; annotation: HRI and RAB.
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                                                                                              Tashiro, H., Yamazaki, M., Watanabe, K., Kumagai, A., Itakura, S., Fukuzumi, Y., Pujimori, Y., Koniyama, M., Sugiyama, T., Irie, R., Otsuki, T., Sato, H., Wakamatsu, A., Ishi, S., Yamanoto, J., Isono, Y., Kawat-Hio, Y., Saito, K., Nishikawa, T., Kimura, K., Yamashita, H., Matsuo, K., Nakamura, Y., Sekine, M., Kikuchi, H., Kanda, K., Wagatesuma, M., Murakawa, K., Kanehori, K., Takahashi-Fujii, A., Oshima, A., Sugiwan, A., Kawakami, B., Suzuki, Y., Sugano, S., Nagahari, K., Masuho, Y., Nagai, K. and Isogai, T., Sugano, S., NEDO, human, CDNa, sequencing project
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Homo sapiens cDNA FLJ10530 fis, clone NT2RP2000985.
AK001392
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/clone lib="UTERU2"
/note="cloning vector: pME18SFL3"
754 c 806 g 623 t
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Pred. No. 5.7e-90;
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Isogai, T. and Yamamoto, J.
Direct Submission
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98.7%;
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121 ACTAATTTCATTTCAAGGCAGTTTTTAAAGAAGTCTTGGAAACAGACGGCGGCACCTTTC
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S Isogai, T. and Otsuki, T. Direct Submission

Submitted (16-FEB-2000) Takao Isogai, Helix Research Institute, Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)

NEDO human cDNA sequencing project supported by Ministry of International Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology; cDNA library construction, 5- & 3-end one pass sequencing and clone selection: Helix Research Institute (supported by Japan Key Technology Center etc.) and Department of Virology, Institute of Medical Science, University of Tokyo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          / translation="MWALCSLLRSAACRTMSQCRTISQAPARRERPRKDPLRHLRTRE
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IELANRPHSAPEYEDFAVVQIPILKENGKGHQPWQSPERPLSPERSPDSESN
ENEPHLHGVSQRRGVENGYRAFICKLHLKRGNFLVLKAKEMGLPVGTAALAPIIA
AVKDGKSITHEGREILAEELCTPPDPGAAFVVVECPDESFIQPICENATFQRYQGKAD
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SSLLRTCDLEEFQTCLVRHCKHAFGCALVHTSGWKVVYSGDTMPCEALVRMGKDATLL
IHEATLEDGLEEEAVEKTHSTTSQAISVGMRMNAEFIMLNHFSQRYAKVPLFSPNFSE
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PRDIEPLLIPSERCKEGPTLSPORVQEGCLLKYQUERREKRORDAITVRNEEFTVBAL
QLPNFQQSVQEYRERAQDGPAREKRSQYPEIIFLGTGSAIPMKIRNVSATLVNISPD
TSLLLDGGEGTFGQLCRHYGDQVDRVLGTLAAVFVSHLHADHHTGLFSILLQRERALA
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                                                                                                                                                                                                        Isogai, T., Ota, T., Hayashi, K., Sugiyama, T., Otsuki, T., Suzuki, Y., Mishikawa, T., Magai, K., Sugano, S., Shiratori, A., Sudo, H., Wagatsuma, M., Hosoiri, T., Kaku, Y., Kodaira, H., Kondo, H., Sugawara, M., Takahashi, M., Chiba, Y., Ishida, S., Murakawa, K., Ono, Y., Takiguchi, S., Watanabe, S., Kimura, K., Murakawi, K., Ishii, S., Kawai, Y., Saito, K., Yamamoto, J., Wakamarsu, K., Nagahari, K., Masuho, Y., Makamura, Y., Magahari, K., Masuho, Y., Minomiya, K. and Iwayanagi, T.
                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/db_xref="taxon:9606"
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/cell_type="teratocarcinoma"
/clone_lib="NT2RP2"
/note="cloning vector: pME18SFL3-mRNA from NT2 neuronal precursor cells after 2-weeks retinoic acid (RA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2676 GGTATGGAGCTGTGCCGAGGCTTGGGGTCCCACATAAGCACTAGTCTATAGATGCCTCTT 2735
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AK001392.1 GI:7022621
oligo capping; fis (full insert sequence).
Homo sapiens teratocarcinoma cell_line:NT2 cDNA to mRNA,
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Best Local Similarity 98.7%; Pred. No. 5.8e-90;
Matches 297; Conservative 0; Mismatches 4.
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/note="unnamed protein product"
                                                                   clone_lib:NT2RP2 clone:NT2RP2000985.
Homo sapiens
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/protein_id="BAA91666.1"
/db_xref="G1:7022622"
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human sequence in NCBI. STSs designed and developed at the Human Genome Center.
Location/Qualifiers
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1 (bases 1 to 429)
Olivier, M. and Cox, D.R.
Unpublished, Olivier, M., Cox, D.R. (2000)
Unpublished, (2000)
                                                                                                                                   2796 ACTAATTTCATTTCAAGGCAGTTTTTAAAGAAGTCATGGAAACAGACGGCGGCGCTTTC
                                                     181 CTCTAATCCAGCAAAGTGATTCCCTGCACACCAGAGACAAGCAGAGTAACAGGATCAGTG
                                                                                            2856 CTCTAATCCAGCAAATGATTCCCTGCACACAGAGACAAGCAGAGTAACAGGATCAGTG
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94 degrees C for 30 s
60 degrees C for 30 s
72 degrees C for 23 s
30
Perkin Elmer 9700
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Primer: each 1 uM
dNTPs: each 200 uM
AmpliTag Gold Polymerase: 0.07 units/ul
Total Vol: 5 ul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Michael Olivier, David R. Cox Stanford Human Genome Center Stanford University School of Medicine 400S Miranda Ave. 2nd Fl., Palo Alto, C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tel: (650) 320-5800
Fax: (650) 320-5801
Email: olivierGebgc.stanford.edu
Primer A: TTTGCTGGATTAGAGGAAGGTG
Primer B: AGTGAAGATCTGGAGACCTGAA
STS size: 322
PCR Profile:
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/map="17"
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Thermal Cycler:
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Gorilla gorilla

Bukaryota; Metazoa; Chordata; Catarthin; Hominidae; Gorilla.

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Tavtigian, S. V., Simard, J., Teng, D.H.F., Abtin, V., Baumgard, M.,

Beck, A., Camp, N.J., Carillo, A.R., Chen, Y., Dayananth, P.,

Ghaffari, S., Gupte, J.S., Hu, R., Iie, P., Janecki, T., Kort, E.N.,

Laity, K.E., Leavitt, A., Leblanc, G., McArthur-Morrison, J.,

Federson, A., Penn, B., Peterson, K.T., Reid, J.E., Richards, S.,

Schroeder, M., Smith, R., Snyder, S.C., Swedlund, B., Swensen, J.,

Thomas, A., Tranchart, M., Woodland, A.M., Labrie, F., Skolnick, M.H.,

Neuhausen, S., Rommens, J. and Cannon-Albright, L.A.

A candidate prostate cancer susceptibility gene at chromosome 17p

21095977
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                                                                                                                                                                                                                                                          299 GGTATGGAGCTGGGCCTTGGGCTCCCACATAAGCACTAGTCTATAGATGCCTCTT 240
                                                                                                                                                                                                                                                                                                    180 ACTAATTTCATTTCAAGGCAGTTTTTAAAGAAGTCATGGAAACAGACGGCGGCACCTTTC 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGTCTAAGTGTCCGAGACTTAACGAAAATAGTATTTCAGCTGCAATAAAGATTGAGTTTG 300
                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       120 CTCTAATCCAGCAAAGTGATTCCCTGCACACAGAGACAAGCAGAGTAACAGGTCAGTG 61
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                                                                                                                                                                                                                     1 GGTATGGAGGTGTGCCGAGGCTTGGGCTCCCACATAAGCACTAGTCTATAGATGCCTCTT
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                                                                                                                                          DB 11; Length 429;
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Unpublished
                                                                                                                                          Score 286.4; DB 11;
Pred. No. 2.4e-87;
0; Mismatches 1;
                                                                                115 t
                                                              .427)
/clone_lib="Human"
106. .427
106. .128
complement (405. .42
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                                                                                108
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                                                                                                                                          Query Match
Best Local Similarity 99.3
Matches 298; Conservative
                                                                              91 a
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AUTHORS
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VERSION
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SOURCE
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                                                                            BASE ČC
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/trānslation="MWALCSLLRSAAGRTWSQGRTISQAPARRERPRKDPLRHLRTRE
KRGPSGCSGGDGNTYVLQVVAAGSRDSGAALYVFSEPRRYLFNGGGVQRLMOGHKLKV
VRLDNIFLTRMHWSNVGLSGMILTLERGTGLPKCVLSGPPGLEKYLEAIKIFSGPLKG
IELAVRPAAFVEDBETMYVYQIPHSGQRGRHQPWQSPBRFLSRLSPERSSDSESN
ENEPHLPHGVSQRRGVRDSSLVVAFICKLHLKRGNFLVLKAKEMGLPVGTAAIAPIIA
                                                                                                                                                                                     Direct Submission
Submitted (27-SBP-2000) Myriad Genetics, Inc., 320 Wakara Way, Salt
Lake City, UT 84103, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AVKDGKS I THEGREILAEELCTPPDPGAAFVVVECPDESFIOPI CENATFQRYGGKAD
APVALVVHMA PESVLVDSRYQQWMERFEPDTOHLVABNCASYNHLKSHKIUTQLNLLI
HPDI FESFCKKEGPTLSVPWQGECLLKYQLERFEWQRDAI I TICNPEEFI VEA
LQDLPPPQSVQEYRRSVQDVPAPAEKSQYPEI I FLGTGSAI PMKI RNVSATLVNI SP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DTSLLLDCGEGTFGQLCRHYGDQVDRVLGTLAAVFVSHLHADHHTGLLNILLQREQAL
ASLGKPLHPLLVVAPSQLKAWLQQYHNQCQEVLHHISMIPAKCLQEGAEISSPAVERL
ISSLLRTCDLEEFQTCLVRHCKHAFGCALVHTSGWKVVYSGDTMPCEALVRMGKDATL
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EKVGVAFDHMKVCFGDFPTMPKLIPPLKALFAGDIEEMEERREKRELRQVRAALLSGE
LAGGLEDGEPQQKRAHTEEPQAKKVRAQ"
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Gupte, J.S., Hu, R., Iliev, D., Janecki, T., Kort, E.N., Laity, K.E., Leavitt, A., Leblanc, G., McArthur-Morrison, J., Pederson, A., Penn, B., Sterson, X., T., Reid, J.E., Richards, S., Schroeder, M., Smith, R., Snyder, S.C., Swedlund, B., Swensen, J., Thomas, A., Tranchant, M., Woodland, A.-M., Labrie, F., Skolnick, M.H., Neuhausen, S., Rommens, J. and Cannon-Albright, L.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 ACTAATTTCATTTCAAGGCAGTTTTTAAAGAAGTCTTGGAAACAGACGGCGGCGCCTTTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'note="similar to Homo sapiens HPC2/ELAC2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
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Pred. No. 4.1e-76;
0; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                 /organism="Gorilla gorilla"
/db_xref="taxon:9593"
1. 2893
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Sequence 42 from Patent WO0102568.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /protein_id="AAG24916.1"
/db_xref="GI:10946489"
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/product="ELAC2"
                                                                                                                                                                                                                                                                                                                                                                                                                                       gene="ELAC2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1. .2481
/gene="ELAC2
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ilarity 93.4%;
Conservative
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Best Local Similarity
Matches 283; Conserv
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FEATURES
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                                                                                  Homo sapiens
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                            (Mases 1 to 386)

Williams, L. T., Escobedo, J., Innis, M. A., Garcia, P. D., Klinger, J.,

Williams, L. T., Escobedo, J., Innis, M. A., Garcia, P. D., Klinger, J.,

Lassam, A., Reinhard, C., Randazzo, F., Kennedy, G.C., Pott, D.,

Labat, I., Leshkowitiz, D., Kita, D., Garcia, V. and Strache-Crain, B.

Human genes and gene expression products

Patent: WO 0102568-A 42 11-JAN-2001;

CHIRON CORPORATION (US); HYSBQ, INC. (US)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia; Eutheria, Primates, Catarrhini, Hominidae; Homo.
1 (bases 1 to 137)
Nang, D.G., Fan, J.B., Siao, C.J., Berno, A., Young, P., Sapolsky, R., Ghandour, G., Perkins, N., Winchester, E., Spencer, J., Kruglyak, L., Stein, L., Topaloglou, T., Hubbell, E., Robinson, E., Mittmann, M., Morris, M.S., Shen, N., Kilburn, D., Rioux, J., Nusbaum, C., Rozen, S., Hudson, T.J., Lipshutz, R., Chee, M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       642927
WIAF-176-STS Human THudson EST Homo sapiens STS cDNA, sequence
tagged site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GTACCCGGGTGGCTTGGAAGAAGTCAGCTCCCGTCGTAGTGAGCACCTCTGGAACCTGTC 463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GTACCCGGGTGGCTTGGAAGAAGTCAGCTCCCGTCGTAGTGAGCACCTCTGGAACCTGTC 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 386;
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Fax: 617 252 1902

Fax: 617 252 1902

Fax: 617 252 1902

Fax: 617 252 1902

Primer A TATTGGAGCTGAAATACTATTTTCG

Primer B: AAGTCATGGAAATACTATTTTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               344 AGGGTCTGCTGTGCACCACCTTGGAGAAGGCTCTCTGTGCTGTAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 158; DB 6; I
Pred. No. 6.3e-43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTCAGAGAGCCACCCTTATTCGCCAAGTCTTTTTGACA 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      464 CTCAGAGAGCCACCCTTATTCGCCAAGTCTTTTGACA 501
                                                                                                                                                                                                                                                                                                                                                                                                                                                           31.5%; Stor. No. 0. 100.0%; Pred. No. 0. Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                            103
                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/db_xref="taxon:9606"
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AX069570
AX069570.1 GI:12579355
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Best Local Similarity 100.
Matches 158; Conservative
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Homo sapiens
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30 _____Thermal Cycler: custom built by IAS, Costar, Cambridge MA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        211 CCAGAGACAAGCAGAGTAACAGGATCAGTGGGTCTAAGTGTCCGAGACTTAACGAAAATA 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        137 AAGTCATGGAAACAGACGGCGGCACCTTTCCTCTAATCCAGCAAANTGATTCCCTGCANA 78
                                                                                                                                                                                                                                                                                                                                                                                     /clone lib="Human THudson EST"
/note="SYSs derived from sequences in dbEST and the Unigene collection."
                           94 degrees C for 4.00 minutes 94 degrees C for 50.0 seconds 58 degrees C for 1.50 minutes 72 degrees C for 1.00 minutes 30
                                                                                                                                                                                                                                                                                                                                    1. .137
/organism="Homo sapiens"
/db xref="taxon:9606"
/map="36.40 cR from top of Chrl7 linkage group"
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 133.4; DB 11; Length 137; Pred. No. 1.5e-34; 0; Mismatches 3; Indels 0;
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each 5 r
4 nM
0.5 U
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                                                                                                                                                                                                                                                   1.5 mM
50 mM
10 mM
                                                            Annealing:
Polymerization:
                                               Denaturation:
                                                                                                                                                                                      Taq Polymerase:
Total Vol:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26.6%;
97.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      271 GTATTTCAGCTGCAATA 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 134; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Presoak:
                                                                                                                                                                                                                                                                                  Tris-HCl:
Gelatin:
                                                                                                                                          Template:
size: 137
Profile:
                                                                                                                                                          Primer:
                                                                                                                                                                                                                         Buffer:
Mg2+:
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primer bind
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OM nucleic

Run on:

Seguence:

Database

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BMSS8S80 AGENCOURT
BG614109 i103g09.x
BF91323 IL3-UT011
AQ096225 HS 3037 A
AGG13922 HOMO SAPI
AIRSO202 USU40f01.Y
BFS89079 nac2900.Y
AIRS1670 zu40f01.x
                                                                                           AQ628850 RPCI-11-4
AQ086239 HS 2171 B
AQ183714 HS_3205_B
AQ34349 RPCI11-12
AQ740452 HS_5502_A
AQ677233 HS_5522_A
AL696113 DKFZp686A
B44892 HS-1060-A1-
AL707132 DKFZp686C
                                                                                                                                                                                                     AZ756633 ev14b07.r
AQ378798 RPCIII-15
AA584125 no10908.s
AL043719 DKFZp434L
                                                                                                                                                                                                                                                                                                                                                A0144748 HS 3092 A
AA478209 zu40f01.r
A0019249 CIT-HSP-2
A058382 RPCI-11-4
A0059714 Pan trogl
BF342636 602013777
                    AC09972 ELT8E10.x
AQ196057 RPC111-58
AQ071874 HS 3018 A
AC084157 Pan trog1
AQ230437 HS 2034 A
B95260 CIT-HSP-217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BF244530 992 bp mRNA linear EST 14-NOV-2000 601862835F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4080393 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                   BM990962 UI-H-DIO-
AV759518 AV759518
AG047439 Pan trogl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1. (bases 1 to 992)

NIH-MGC http://mgc.nci.nih.gov/.

National institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conteact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Proturement: ATC
CDNA Library Preparation: CLONETECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM940 row: f column: 10
High quality sequence stop: 328.
Location/Qualifiers
rce
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                                                                                                                                                      AQ677233
AL696113
B44892
AL707132
AZ756633
AQ378798
AA584125
AL043719
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BQ614109
BF913236
AQ096225
AG013922
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BF589079
A1821670
                                                                                                                                                                                                                                                                                                                                                                            AQ019249
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mRNA sequence.
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1115.6
1115.6
1115.4
1115.4
1115.2
1115.2
1115.2
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AUTHORS
TITLE
JOURNAL
COMMENT
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BF244530 601862835
BG943515 ax38g05.x
AG177687 Pan trogl
AQ742365 HS 5382_B
AQ587593 CITBI-EI-
AQ587553 CITBI-EI-
                                                                              May 17, 2003, 15:56:54; Search time 680.481 Seconds (without alignments) 11900.029 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                       1 tatcaggtgactgaattcta......aagctctgagggactgacgt 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Description
                                                                                                                                                                                                                                          32308132
          version 5.1.5
- 2003 Compugen Ltd.
                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                 16154066 segs, 8097743376 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUMMARIES
                                                                                                                                                                                                                                                                                               Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                        nucleic search, using sw model
                                                                                                                           US-09-434-382-28_COPY_1_500
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BG943515
AG177687
AQ742365
AQ587593
AQ587553
                                                                                                                                                                            IDENTITY NUC
Gapop 10.0 , Gapext 1.0
          GenCore
Copyright (c) 1993
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gb_htc:*
gb_htc:*
gb_est4:.*
gb_est5:*
em_est6nn:*
em_est6nn:*
em_gss.*:
em_gss_inv:*
em_gss_inv:*
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em_gss_fun:*
em_gss_mam:*
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Maximum DB seq length: 200000000
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em_gss_other
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em_estin: *
em_esteru: *
em_estpy: *
em_estppl: *
em_ettpl: *
em_ttc: *
gb_estl: *
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119.6
118.2
118.2
117.8
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(bases 1 to 669)
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Matches 140; Conserv
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SOURCE
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AG177687
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                                               /clone='IMAGE:4000.55"
/clone=Inb="IMAGE:4000.55"
/tissue_type="glioblastoma"
/lab_host="NIHH MGC_55"
/lab_host="DH10B (TI phage-resistant)"
/lab_host="DH10B (TI phage-resistant)"
/note="organ: brain; Vector: pDNR-LIB (clontech); Site_I:
Sfil (ggccgctcggcc); Site_2: Sfil (ggccattatggcc);
Double-stranded cDNA was prepared from cell line RNA.
adaptors were used in cloning as follows: S'
adaptors were used in cloning as follows: S'
adaptors were used in cloning as follows: S'
adaptor sequence: S'-ARCGCCGCAATATGGCC-3' and 3' adaptor
sequence: S'-ATTTAGAGGCCGAGGCCCAATGGTGC-4T(3) BN-3'
(where B = A, C, or G and N = A, C, G, or T). Average
insert size 1.55 kb (range 0.9-4.0 kb). 12/15 colonies
contained inserts by PCR. This library was enriched for
full-length clones and was constructed by Clontech
Laboratories (Palo Alto, CA)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BG943515 546 bp mRNA linear EST 11-JUN-2001 ax38g05.x1 Proliferating Human Erythroid Cells (LCB:ax library) Homo sapiens cDNA clone ax38g05 random, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Jeffery L. Miller
Laboratory of Chemical Biology
National Institute of Diabetes and Digestive and Kidney Diseases
Building 10, Room 9817, National Institutes of Health, Bethesda, MD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo. I (bases I to 546)
Gubin,A.N., Njoroge,J.M., Bouffard,G.G. and Miller,J.L. Gene expression in proliferating human erythroid cells Genomics 59 (2), 168-177 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="Proliferating Human Erythroid Cells (LCB:ax librar\vec{y})"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181 TTTTTGTTTTGTTTTTGTTTTGAGACAGGGTCTCGAGGTGTCACCCAGGCTGGAGT 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                241 GCAGTGGCGCGATTTCGACTCACCGCAACCTCCGCCTTCGCGCTTAAGCGATTCTCCTGC 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   309 TTTTTTTTTTTTTTTTTTTTTTTTTTTGGACACAGAGTCTCGCTCTGTCGCGCAGGCTGGAGT 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: jm7f@nih.gov
DNA Sequencing and analyses by National Institutes of Health
Intramural Sequencing Center (NISC).
Plate: 38 row: g column: 05
Seq primer: -21M13 forward primer (ABI).
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         249 GCAGTGGCGCGATCTCGGCTCACTGCAACCTCTGCCTCCGAGTTCAAGCGATTCTCTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ·.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             24.5%; Score 122.4; DB 12; Length 992; 84.1%; Pred. No. 1e-13; ive 0; Mismatches 26; Indels 0;
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/organism="Homo sapiens"
/db_xref="taxon:9606"
organism="Homo sapiens"
                     /db_xref="taxon:9606"
/clone="IMAGE:4080393"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BG943515.1 GI:14342887
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Fax: 301 435 5148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 138; Conservative
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/Incte="Core and a blood; Vector: Lambda ZAP II; Site 1: ECORI; Site 2: ECORI; 65,000 proliferating erythroid cells from the buffy coat of a blood donation were obtained by flow cytometric separation after a 5-day culture period in the presence of erythropoietin. Total RNA was purified from the sorted cell population using TRIzol reagent. RNA (0.3 ug) was converted into double stranded cDNA using Clontech's Caprinder CDNA Library Construction Kit (Clontech) according to the manufacturer's protocol and cloned into EcoRI digested Lambda Zap II vector (Stratagene). The phage library was amplified once prior to in vivo excision in SOLR cells. Individual colonies were grown, and the cDNA inserts were sequenced in high throughput (NIH intramural sequencing center http://www.nisc.nih.gov/).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbes@gsc.riken.go.jp, Wit:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library RPCI-43 This BAC end was generated during the R&D process and may have higher chance of clone tracking errors.
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Pan troglodytes DNA, clone: RP43-049G22.TJ, genomic survey
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Bub troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181 TITITGITITGITTTGITTTGTTTTGAGACAGGGTCTCGAGGTGTCACCCAGGCTGGAGT
                                                                       /cell_line="Primary Culture of Peripheral Blood
Monomuclear Cells"
/dev stage="Progenitor; EPO responsive CD71++++"
/lab_host="SOLR"
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Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.
BAC end sequences of Library RPCI-43
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                301 CTCAGCCTCCCAAGTAGCTGGGACTACAAGCTCGGGACACCACGTAAAAATGAT 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   127 CTCGGCCTCCCGAGTAGCTGGGATTACACAGGTGTGCCACCATGCCCAACTAAT 180
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Pred. No. 4.3e-13;
0; Mismatches 34
                                       /cell_lipe="Erythroid Cells"
/cell_line="Primary Culture
type="blood"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AG177687.1 GI:16707367
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80.5%;
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Location/Qualifiers
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Matches 173;
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AQ587593/c
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VERSION
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                 FEATURES
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High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-388
Tel: (206) 616-388
Fax: (206) 616-3887
Email: jwallacc@u washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
or from Resear h Genetics (info@resgen.com). BAC end Web Server:
Plate: 958 row: D column: 15
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HS_5382_B1_B08_T7A RPCI-11 Human Male BAC Library Homo sapiens
genomic clone Plate=958 Col=15 Row=D, DNA sequence.
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Adams, M.D. and
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (Dases 1 to 811)
Mahairas,G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. an
                                                                                                                                                                                                                                                                                                                                                                   TTGTTTTGTTTTGAGA 209
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                                                                                                                                                                                                                                                                                                                                                                                                                                       210 CAGGGTCTCGAGGTGTCACCCAGGCTGGAGTGCAGTGGCGCGATTTCGACTCACCGCAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       177 redadricteacreretereceadecredadrecadrecerearerrecereace
                                                                                                                                                                            /sex="male"
/cell_type="lymphocytes"
/clone_lib="RPCI-43 Chimpanzee Male BAC Library"
: 146 c 130 g 233 t
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                                                                                                                                                                                                                                                                                           Length 669;
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                                                                                                                                                                                                                                                                                                                                                                 organism="Pan troglodytes"
                                                                                                                                          /db_xref="taxon:9598"
/clone="RP43-049G22.TJ"
                                                                                       Location/Qualifiers
                                  pBACe3.6
EcoRI
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                                                                      : ECORI
Sequencing: TJ
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R.Site 2
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KEYWORDS
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 399)
S Zhao,S., Adams,M.D., Nierman,W., Malek,J., Shizuya,H., Simon,M. and Venter,J.C.
Use of BAC End Sequences from CalTech Libraries for Sequence-Ready Map Building
Unpublished (1997)
Other_GSSs: CITB1-E1-2643H8.TF
Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Fax: 301 838 0200
Fax: 101 838 0200
                                                                                                                                                                                                                                                                                                                                                                                         /note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI; Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at EcoRI sites" 43 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seg primer: M13 Reverse
Class: BAC ends.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              131 CTTTAGAGCTTGTCCTCTATTCTTGCTTTTCTTTCCAAAAAACACTACAATTTTTGTTTT 190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 17; Length 811;
                                                                                                        /organism="Homo sapiens"
/db xref="taxon:9606"
/clone="plate=958 Col=15 Row=D"
/clone=lib="RPCI-11 Human Male BAC Library"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23.6%; Score 118.2; DB 17; Length ilarity 70.0%; Pred. No. 6.9e-13; Conservative 0; Mismatches 73; Indels
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CITBI-E1-2643H8.TR CITBI-E1 Homo
Location/Qualifiers
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AU121896 MAMMAI Homo sapiens cDNA clone MAMMAI001220 5', mRNA
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (Dases 1 to 727)
Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y.,
Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bmail: genomics@hri.co.jp
HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
Location/Qualifiers
                                                                                                                                                                                                                                                        339 TITITITITITITITITITITIGAGAIGGAGTCTIGCTCTGTCACCCAGGCTGGAGTGCAG
                                                                                                                                                                                                                                                                                                                                   279 TGGCGCGATCTCGGCTCACTGCAAGCTCCGCCTCCCAGGTTCACGCCATTCTCCTGCCTC 220
                                                                                                                                                       CICITGCITTAGAGCITGTCCTCTATTCTTGCTTTTCCAAAAAACACTACAATTTT 184
                                                                                                                                                                                           399 CTCTCCCTTCAAATATCAACATTCTACAATAGAGGCATCCAGAGAATGACAACCTTTTT 340
                                                                                                                                                                                                                                                                                                               TGGCGCGATTTCGACTCACCGCAACCTCCGCCTCCGCGCTT-AAGCGATTCTCTCCTGCCTC 303
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                                                                                                                                                                                                                                    TGTTTTGTTTTGTTTTGTTTTGAGACAGGGTCTCGAGGTGTCACCCCAGGCTGGAGTGCAG
                                                                              Length 450;
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1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
TTE1: 81-438-52-3975
Fax: 81-438-52-3986
                                                                                                                                                                                                                                                                                                                                                                                           304 AGCCTCCCAAGTAGCTGGGACTACAAGCTCGGGACACCACG 344
                                                                                                                                                                                                                                                                                                                                                                                                                AGCCTCCCAAGTAGCTGGGACTACAGGCACCCGCCACCATG 179
                                                                              DB 17;
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                                                                            23.6%; Score 117.8; DB 73.8%; Pred. No. 1e-12;
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/tissue type="mammary gland"
/note="Vector: pME185FL3"
159 c 146 g 248 t
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                                                                                                                 0; Mismatches
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Human BAC Library
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/clone="MAMMA1001220"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AU121896.1 GI:10937131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     human cDNA project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23.6%;
ilarity 73.8%;
Conservative 0
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Genomics Laboratory
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CalTech F
                                                                                                                   Conservative
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Best Local Similarity
Matches 163; Conserv
                                                                                                Similarity
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                                                                              Query Match
Best Local
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AU121896
LOCUS
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KEYWORDS
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Bukaryotra; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

1 (bases 1 to 450)

2 Zhao, S., Adams, M.D., Nierman, W., Malek, J., Shizuya, H., Simon, M. and Venter, J.C.

Use of End End Sequences from CalTech Libraries for Sequence-Ready

Map Building

Unpublished (1997)

Other GSSs: CITELE1-2643H14.TF

Contact: Shaying Zhao, William Nierman, Mark Adams

Department of Eukaryotic Genomics

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850

Tel: 301 838 0200

Fax: 301 838 0208

Email: hbe@tigr.org

Clones are available from Research Genetics (info@resgen.com). BAC

end search page:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AQS87553 450 bp DNA linear GSS 07-JUN-1999
CITBI-E1-2643H14.TR CITBI-E1 Homo sapiens genomic clone 2643H14,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seg primer: M13 Reverse
Class: BAC ends.
                                                                                                         /Betal type="sperm"
/call type="sperm"
/note="Vector: pBeloBACll; Site_1: EcoRI; Site_2: EcoRI;
calTech Human BAC Library D"
a 83 c 108 g 89 t
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/note="Vector: pBeloBAC11; Site_1: BcoR1; Site_2: BcoR1;
                                                                                                                                                                                                                                                                                                                                                                                                                    399 CTCTCCCTTCAAATATCAACATTTCTACAATAGAGGCATACAGAGAATGACAACCTTTTT 340
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H
                                                                                                                                                                                                                                    Length 399;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   304 AGCCTCCCAAGTAGCTGGGACTACAAGCTCGGGACACCACG 344
                                                                                                                                                                                                                                    DB 17;
                                                                                                                                                                                                                                  Score 117.8; DB Pred. No. 1e-12; 0; Mismatches
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/db_xref="taxon:9606"
/clone="5643H14"
/clone lib="CITBI-EI"
/sex="male"
  1. .399
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/db_xref="taxon:9606"
/clone="2643H8"
                                                                          /clone_lib="CITBI-E1"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
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AQ587553.1 GI:5014233
GSS.
                                                                                                                                                                                                                                    23.6%;
73.8%;
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Best Local Similarity 73.8
Matches 163; Conservative
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AQ587553/c
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Gaps

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304 AGCCTCCCAAGTAGCTGGGACTACAAGCTCGGGACACCACG 344

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185

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Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Herbert Morse, M.D., Michael R. Emmert-Buck,

M.D., Ph.D.

CDNA Library Preparation: David B. Krizman, Ph.D.

CDNA Library Preparation: David B. Krizman, Ph.D.

DNA Sequencing by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CCAP clone distribution information can be

found through the I.M.A.G.B. Consortium/LINL at:

www-bio.llnl.gov/bbrp/image/image.html

Seq primer: -40UP from Gibco.

Location/Qualifiers
                                                                                                                                            A1609972

tr78cl0.xl NCI CGAP HSC3 Homo sapiens cDNA clone IMAGE:2246898 3'
similar to contains Alu repetitive element; contains element MER9
repetitive element; mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GSS 20-APR-1999
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 415)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Organ: bone marrow; Vector: pAMP1; mRNA made from lymphoid tissue, cDNA made by oligo-dr priming. Directionally cloned. Size-selected on agarcse average insert size 500 bp. Primary library, non-amplified. CDNA Library Preparation: David B. Krizman, ph.D. Reference: Krizman et al. (1996) Cancer Research 56:5380-5383.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
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/clone="IMAGE:2246898"
/clone_lib="NCI_CGAP_HSC3"
/tissue_type="CD34+, T negative, patient with chronic myelogenous leukemia"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               172 ACACTACAATTTTTGTTTTGTTTTGTTTTGAGACAGGGTCTCGAGGTGTCACCCA 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        412 ATACGACTTTTTTTTTTTTTTTTTTTTTGAGACAGAGTCTCGCTGTTTCATCCA 353
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0; Mismatches 34
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Best Local Similarity
Matches 138; Conserv
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TITLE
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,

Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

1 (bases 1 to 770)

Evans, G.A., Burbee, D., Davies, C., Hahner, L., Oliver, T., Gilbert, M.,
Jones, D., Ward, T., Gillilan, E., Schagemann, J., Probst, S., Harris
, J., DePord, J., McFarland, J., Burzinski, K., Khan, M., Kupfer, K. and
Garner, H.R.
                                                                                                                                                                                                                                                                                                                               B02308 13-JUL-15
CSRL-151D1-u CSRL flow sorted Chromosome 11 specific cosmid Homo
sapiens genomic clone CSRL-151D1, DNA sequence.
                                              431
                                                                                         303
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              270 TTTCTTTTTTTTTTTTTTGGACAGAGTCTCGCTCTGTCGCGCAGGCTGGAGTGCA 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            244 GIGGCGCGATTICGACTCACCGCAACCICCGCCTCCGCGCTTAAGCGATTCTCCTGCCTC 303
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/db_xref="taxon:9606"
/clone="cSRL-151D1"
/clone_lib="cSRL flow sorted Chromosome 11 specific
TGTTTTGTTTTGTTTTGTTTTGAGACAGGGTCTCGAGGTGTCACCCAGGCTGGAGGTGCAG
                                                                                                                              432 TGACGCGATCTCGGCTCACTGCAAGCTCGGCCTCCCAGGTTCACGCCGTTTTCCTGCCTC
                                         372 TGTTGTTTTTTTTTTTTTTGAGAGAGTCTCTCTCTGTCACCCAGGCTGGAGTGCAG
                                                                                     TGGCGCGATTTCGACTCACCGCCAACCTCCGCCTT-AAGCGATTCTCCTGCCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genomic Sequence Sampled Map of Chromosome 11
Unpublished (1996)
Contact: Evans GA, Shane Probst
MCDermott Center for Human Growth and Development
University of Texas Southwestern Medical Center At Dallas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: gevans@utsw.swmed.edu, shane@mcdermott.swmed.edu
PCR PRimers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 17; Length 770;
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Pred. No. 8.4e-13;
0; Mismatches 27; Indels
                                                                                                                                                                          304 AGCCTCCCAAGTAGCTGGGACTACAAGCTCGGGACACCACG 344
                                                                                                                                                                                                 High quality sequence stop: 770.
Location/Qualifiers
1. .770
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 23.6%;
Best Local Similarity 83.2%;
Matches 134; Conservative
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E. 1 (Bases I to 669)

S. Adams, M.D., Rounsley, S.D., Zhao, S., Bass, S., Linher, K., Golden, K., Berry, K., Granger, D., Suh, B., Wible, C., de Jong, P. and Venter, J.C.

Use of human BAC End Sequences for Sequence-Ready Map Building

Unpublished (1998)

Other GSSs: RPCIII-58GII.TK

Contact: Mark Adams

Department of Eukaryotic Genomics

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850, USA

Tel: 301 838 0208
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: mdadams@tigr.org
Clones are derived from the human BAC library RPCI-11. For BAC
Library availability, please contact Pieter de Jong
(pieter@dejong med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
Research Genetics (info@resgen.com). BAC end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
Class: BAC ends.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amamalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (Dases 1 to 389)
RPCI11-58G11.TJ RPCI-11 Homo sapiens genomic clone RPCI-11-58G11,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /cell_type="Lymphocytes"
/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
RPCIll Human Male BAC Library"
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|db_xref="taxon:9606"
|clone="RPCI-11-58G11"
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/sex="Male"
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Pan troglodytes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AGU84157 654 bp DNA linear GSS 03-NOV-200
Pan troglodytes DNA, clone: PTB-081N03.F, genomic survey sequence.
AG084157
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Pan.
Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. &
Hood,L.
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B-Coli DH10B"
115 c 87 g 118 t
                                                                                                Sequence-tagged connectors: A sequence approach to mapping and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1. .389
/organism="Homo sapiens".
/db xref="taxon:9606".
/clone="Plate=3018 Col=10 Row=I"
/clone lib="CIT Approved Human Genomic Sperm Library
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            238 AGTGCAGTGGCGCGATTTCGACTCACCGCAACCTCCGCCTTCGCGCTTAAGCGATTCTCC 297
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Direct Submission
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                                                                                                                               scanning the human genome
Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
                                                                                                                                                                                                                                                                                          USA
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                                                                                                                                                                                                                                High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109,
Tel: (206) 616-3618
Fax: (206) 616-3887
                                                                                                                                                                                                       Contact: Mahairas GG, Wallace JC, Hood L
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                                                                                                                                                                                                                                                                                                                                                                    Email: jwallace@u.washington.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             High quality sequence stop: 389.
Location/Qualifiers
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Plate: 3018 row: I column: 10
Class: BAC ends
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Best Local Similarity 81.4%;
Matches 136; Conservative 0
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HS_2034_A2_F03_MR_CIT_Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2034 Col=6 Row=K, DNA sequence.
AQ230437
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GSS.
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 312)

Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T.,

Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
Clones are derived from the chimpanzee BAC library PTB This BAC was generated during the R&D process and may have higher chance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome
Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                      348 chadchchadahadahadahadahadhiriririririririririridadaha 289
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                                                                                                                                                                                                                                                                                                                                                                                                          RGTTTTGTTTTGAGACA 211
                                                                                                                                                                                                                                                                                                                                                                           Gaps
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0
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                                                                                                                                                                                                                         /cloue- . . . /cell_type="lymphoblast" /cell_type="lymphoblast" /clone_lib="PTB_Chimpanzee_Male_BAC_Library" /4\overline{6} c 143 g 156 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Mahairas GG, Wallace JC, Hood L, Halp Throughput Sequencing Center University of Washington 401 Queen Anne Avenue North, Seattle, WA 98109, USA 1911: (206) 616-3887 Fax: (206) 616-3887 Email: jwallace@u.washington.edu
                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                           47;
                                                                                                                                                                                                                                                                                                                                      Query Match
23.4%; Score 116.8; DB 1
Best Local Similarity 75.5%; Pred. No. 1.4e-12;
Matches 145; Conservative 0; Mismatches 47
                                                                                                                                                                   1. .654
/organism="Pan troglodytes"
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/clone="PTB-081N03.F"
                                                                                                                                                                                                                                                                                                                                                                                                        CITGCITITCTTTCCAAAAAACACIACAATITITGITI
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Plate: 2034 row: K column: 6
Class: BAC ends
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R.Site 1 : SacI
R.Site 2 : SacI.
                                                                     Sequencing: -21M13
                                      clone tracking errors.
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COMMENT
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AQ230437
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Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Joses 1 to 389)

S Adams, M.D., Rounsley, S.D., Zhao, S., Field, C.E., Bass, S., Linher, K., Golden, K., Barry, K., Granger, D., Suh, E., Wible, C., Shizuya, H., Simon, M. and Venter, J.C.

Use of a random BAC End Sequence Database for Sequence-Ready Map

Building (1988)

VL Dublished (1998)

Other GSSs: CIT-HSP-2171L9. TF

Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200

Fax: 301 838 0200

Email: mdadams@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
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Seg primer: M13 Reverse
Class: BAC ends.
1. .312
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/clone="Plate=2034 Col=6 Row=K"
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/sex="male"
                                                                                                                                                                /note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in E-Coli DH10B"
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                                                                                                                                                                                                                                                                                               23.3%; Score 116.6; DB 17; Length 312; 78.6%; Pred. No. 1.9e-12; ive 0; Mismatches 40; Indels 1;
                                                                                                                                                                                                                   109 t
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/organism="Homo sapiens'
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/db_xref="taxon:9606"
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B95260.1 GI:2977597
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RPCI-11-479118.TJ RPCI-11 Homo sapiens genomic clone RPCI-11-479118
, DNA sequence.
AQ628850.1 GI:5091242
                                                                                                                                    1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 418)
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/note="Vector: pBACe3.6; Site 1: EcoRI; Site_2: EcoRI;
RPCI11 Human Male BAC Library"
8 84 c 78 g 153 t 53
                                                                                                                                                                                                                                                                                                                          272 CCGCCT-CCGCGCTTAAGGATTCTCCTGCCTCCAGCTCCCAAGTAGCTGGGACTACAAG 330 242 CCGCCTCCCGGGTTCACGCCATTCTCCTGCCTCCAGCTCCCGTGTAGCTGGGACTACAGG 301
                                                                                                                                                                                                                                                                        GAGTTTCGCTCTGTCGCCCCAGGCTGCAGTGCGCGCGATCTCGACTCCCACTGCAAGCT 241
                                                                                                                                                                      212 GGGTCTCGAGGTGTCACCCAGGCTGGAGTGCAGTGGCGCGATTTCGACTCACCGCAACCT 271
                                                                                                                                                                                                              Gaps
/note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
                                                                                                                                    1;
                                                                                            Length 389;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (1997)
Contact: Shaying Zhao, William Nierman, Mark Adams
Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
The Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                  41; Indels
                                                                                          DB 17;
                                                                                          Score 116.4; DB 1
Pred. No. 1.9e-12;
                                                                                                                                  0; Mismatches
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/db_xref="GDB:7683761"
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/clone lib="RPCI-11"
/sex="Male"
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Best Local Similarity 78.4
Matches 152; Conservative
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COMMENT
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Search completed: May 17, 2003, 18:18:14 Job time : 687.481 secs Sequence 1404, Ap Sequence 1404, Ap Sequence 1404, Ap Sequence 7825, Ap Sequence 7, Appli Sequence 1076, Ap

Sequence 1077, Ap Sequence 1077, Ap

Sequence 9422, Ap Sequence 3, Appli Sequence 86, Appl Sequence 90, Appl Sequence 87, Appl Sequence 87, Appl

Sequence 3133, Ap Sequence 326, App Sequence 327, App

Sequence 326,

Sequence 9139, Sequence 327 Sequence 327

Sequence 715, Sequence

Minimum DB seq Maximum DB seq

Database

Perfect score:

Sequence:

OM nucleic -

Run on:

Scoring table:

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APPLICANT: Tavidian, Sean V.
APPLICANT: Tavidian, Sean V.
APPLICANT: Tavidian, Sean V.
APPLICANT: Tavidian, Sanard, Jacques
APPLICANT: Simard, Jacques
APPLICANT: Rommens, Johanna M.
APPLICANT: Rommens, Johanna M.
APPLICANT: Myriad Genetics, Inc.
TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility
TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes
TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes
FILE REFERENCE: 2318-258
CURRENT FILIANG DATE: 2000-11-20
RIOR APPLICATION NUMBER: US 60/107, 468
PRIOR PILING DATE: 1998-11-06
PRIOR PILING DATE: 1998-11-06
PRIOR FILING DATE: 1999-11-05
PRIOR FILING DATE: 1999-11-05
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LOCATION: (9107..(13104)
COTHER INFORMATION: exon 1: 3105-3089; exon 3:
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OTHER INFORMATION: exon 6: 5582-5650; exon 7: 7075-7194; exon 8:
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US-09-764-860-1075
US-09-946-807-1404
US-09-795-686-1404
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US-09-764-891-7825
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US-10-074-095-1077
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US-09-764-8177-3132
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US-09-795-668-327
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US-09-795-686-327
US-10-091-572-715
US-10-091-572-715
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ORGANISM: Homo sapiens
FEATURE:
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LENGTH: 26664
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     Sequence 8718, Ap
Sequence 8719, Ap
Sequence 78, Appl
Sequence 146, App
Sequence 3, Appli
Sequence 3, Appli
Sequence 1, Appli
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Sequence 943, App
Sequence 944, App
Sequence 1075, Ap
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10174.595 Million cell updates/sec
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Sequence 28, Appl
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APPLICANT: Tartigian, Sean V.
APPLICANT: Teng, David H.F.
APPLICANT: Simard, Jacques
APPLICANT: Simard, Jacques
APPLICANT: Rommens, Johanna M.
APPLICANT: Rommens, Johanna M.
APPLICANT: Myriad Genetics, Inc.
TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes
FILE REFERENCE: 2318-258
CURRENT APPLICATION NUMBER: US/09/988,687
CURRENT PILING DATE: 2001-11-20
PRIOR APPLICATION NUMBER: 09/564,805
PRIOR FILING DATE: 2000-05-05
PRIOR FILING DATE: 2000-05-05
PRIOR FILING DATE: 1998-11-06
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                 OTHER INFORMATION: exon 19: 21045-21154; exon 20: 21795-21895; exon OTHER INFORMATION: 21: 23973-24093; exon 22: 24354-24432; exon 23: OTHER INFORMATION: 21: 23973-24093; exon 22: 24354-24432; exon 23: OTHER INFORMATION: signal: 26447-26452

NAME/KEY: variation
LOCATION: (226).. (23879)
OTHER INFORMATION: positions 826 and 23180 is G or C; y at OTHER INFORMATION: scriptions 1914, 5568, 7165, 16431, 1857 and 20486 OTHER INFORMATION: is C or T; n at position 13128 is t or tgat; r at OTHER INFORMATION: positions 22211 and 23879 is A or G.
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Publication No. US20030045704A1
GENERAL INFORMATION:
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US-09-988-687-28
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OTHER INFORMATION: 25026-2...
OTHER INFORMATION: signal: 26447-2643.
OTHER INFORMATION: signal: 26447-2643.
OTHER INFORMATION: signal: 26447-2643.
COTHER INFORMATION: at positions 826 and 23180 is G or C; y at OTHER INFORMATION: positions 1914, 5568, 7165, 16431, 1857 and 20486; OTHER INFORMATION: positions 1914, 5568, 7165, 16431, 1857 and 20486; OTHER INFORMATION: positions 22211 and 23879 is A or G.

OTHER INFORMATION: positions 22211 and 23879 is A or G.

OTHER INFORMATION: positions 22211 and 23879 is A or G.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 TAICAGGIGACTGAATTCTATATTCTGAAGTAGGAGAATACTGTTATTACAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 TITACACATAAGAAAGCTGAGGCTCTGAGAGGTCAAGATCACGCAGCTAACAAATGAGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TTTTGTTTTGTTTTGTTTTGTTTTGAGAGAGAGGTCTCGAGGTGTCACCCAGGCTGGAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GCAGTGGCGCGATTTCGACTCACCGCAACCTCCGCCCTCCGCGCTTAAGCGATTCTCCTGC
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PRIOR APPLICATION NUMBER: 09/.
PRIOR FILING DATE: 1999-11-05
NUMBER OF SEQ ID NOS: 240
SOFTWARE: PATENTIN Ver. 2.0
                                                                                                                                       sapiens
                                                                                                                TYPE: DNA
ORGANISM: Homo
                                                                            SEQ ID NO 28
                                                                                                                                                       FEATURE:
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166 CAAAAAACACTACAATTTTTGTTTTGTTTTGTTTTTGAGACAGGGTCTCGAGGTGT 225
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APPLICANT: Steinthorsdottir, Valgerdur
APPLICANT: Steinthorsdottir, Valgerdur
APPLICANT: Glincher, Jeffrey, R.
TITLE OF INVENTION: HUMAN SCHIZOPHRENIA GENE
FILE REFERENCE: 2345.2004-001
CURRENT APPLICATION NUMBER: US/09/795,668
CURRENT APPLICATION NUMBER: US 09/515,716
PRIOR FILING DATE: 2000-02-28
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OTHER INFORMATION: n=a or g or c or t/u
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LOCATION: (1).7.(1531)
OTHER INFORMATION: h=a or c or t/u
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LOCATION: (1)...(1531)
OTHER INFORMATION: d=a or g or t/u
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; Patent No. US20020045577A1
; GENERAL INFORMATION:
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OTHER INFORMATION: v=a or g or
                                                      COCATION: (1)...(1531)

THER INFORMATION: y=t/u or c
                                                                                                                                                                                                                 NAME/KEY: misc_feature
LOCATION: (1)...(1531)
OTHER INFORMATION: k=g or t/u
                                                                                                                                                                                                                                                                                                            NAME/KEY: misc feature
LOCATION: (1)...(1531)
OTHER INFORMATION: s=g or c
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                                                                                                                      NAME/KEY: misc feature
LOCATION: (1)...(1531)
OTHER INFORMATION: m=a
FEATURE:
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OTHER INFORMATION: w=a
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OTHER INFORMATION: b=g
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NAME/KEY: misc_feature
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                                'KEY: misc_feature
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Matches 149;
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US-09-795-668-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      124 ACTCTTGCTTTAGAGCTTGTCCTCTATTCTTTCTTTTCCAAAAAACACTACAATTT 183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24.1%; Score 120.4; DB 10; Length 7680; 74.3%; Pred. No. 9.5e-24; ive 0; Mismatches 56; Indels 1;
                                                                                                                                  Sequence 3, Application US/09939581A

Sequence 3, Application US/09939581A

GENERAL INFORMATION:
APPLICANT: Hermeking, Heiko
APPLICANT: Kenneth
TILE OF INVENTION: 14-3-3 SIGMA ARREST THE CELL CYCLE
FILE REFERENCE: 1107, 77810
CURRENT APPLICATION NUMBER: US/09/939,581A
CURRENT APPLICATION NUMBER: 09/210,748
PRIOR APPLICATION NUMBER: 09/210,748
PRIOR FILING DATE: 2001-08-28
PRIOR FILING DATE: 1999-12-15
NUMBER OF SEQ ID NOS: 18
SOOTWARE: FASTSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CAGCCTCCCGAGTAGCTGGGACTACAGGCATGTGCCACCATG 6107
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APPLICANT: Stefansson, Hreinn
APPLICANT: Stefansson, Hreinn
APPLICANT: Stefanson, Hreinn
APPLICANT: Guicher, Jeffrey R.
TITLE OF INVENTION: HUMAN SCHIZOPHRENIA GENE
FILE REFERENCE: 2345.2004-001
CURRENT FILING DATE: 2001-09-05
PRIOR APPLICATION NUMBER: US/09/946,807
CURRENT FILING DATE: 2001-09-05
PRIOR APPLICATION NUMBER: US/09/795,668
PRIOR APPLICATION NUMBER: US 09/515,716
PRIOR FILING DATE: 2000-02-28
NUMBER OF SEQ ID NOS: 1531
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 1503841
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Patent No. US20020165144A1
481 AAGCTCTGAGGGACTGACGT 500
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LOCATION: (1)...(1531)
OTHER INFORMATION: r=g or a
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Matches 165; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Homo sapiens
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LENGTH: 7680
                                                                                                                      -09-939-581A-3
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US-09-946-807-1
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                                            SEQ ID NO 1
                                                                                                                                                                                  LOCATION:
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NUMBER OF
SOFTWARE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 120, DB 10, Length 1503841;
Pred. No. 2.4e-22;
0; Mismatches 30; Indels 1;
NUMBER OF SEQ ID NOS: 1531
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; LOCATION: (1)....(1531)
; OTHER INFORMATION: n=a or g or c or t/u
US-09-795-668-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc feature
LOCATION: (1).7.(1531)
OTHER INFORMATION: b=g or c or t/u
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OTHER INFORMATION: h=a or c or t/u
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    or t/u
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                                                                                                                                                                                                                                                                                                            LOCATION: (1) ... (1531)
COTHER INFORMATION: m=a or c
NAME/KEY: misc_feature
LOCATION: (1) ... (1531)
OTHER INFORMATION: k=g or t/u
NAME/KEY: misc_feature
LOCATION: (1) ... (1531)
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LOCATION: (1)...(1531)
OTHER INFORMATION: v=a or g or
NAME/KEY: misc feature
                                                                                                                                                                         LOCATION: (1)...(1531)
OTHER INFORMATION: r=g or a
NAME/KEY: misc feature
LOCATION: (1)...(1531)
OTHER INFORMATION: y=t/u or c
NAME/KEY: misc feature
LOCATION: (1)...(1531)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc_feature
LOCATION: (1)...(1531)
OTHER INFORMATION: w=a or t/u
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 82.8%;
Matches 149; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: (1)...(1531)
OTHER INFORMATION: s=g or c
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                                                                                      TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                        NAME/KEY: misc_feature
LOCATION: (1)...(1531)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc_feature
LOCATION: (1)...(1531)
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                                                                 LENGTH: 1503841
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US-09-795-686-1
                                          SEQ ID NO 1
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APPLICANT: Stefansson, Hreinn
APPLICANT: Steinthorsdottir, Valgerdur
APPLICANT: Gulcher, Jeffrey R.
TITLE OF INVENTION: HUMAN SCHIZOPHRENIA GENE
FILE REFERENCE: 2345.2005-001
CURRENT APPLICATION NUMBER: US/09/795,686
CURRENT APPLICATION NUMBER: 2001-02-28
PRIOR APPLICATION NUMBER: US 09/515,715
PRIOR FILING DATE: 2000-02-28

GENERAL INFORMATION

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Db 532425 CGCCCAGGCTGGAGTGCAGTGGCGGGATCTCGGCTCACTGCAAGCTCCGCCTCCGGGGTT 532484
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 120; DB 10; Length 1503841;
Pred. No. 2.4e-22;
0; Mismatches 30; Indels 1;
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TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PCO06
CURRENT APPLICATION NUMBER: US/09/764,891
CURRENT FILING DATE: 2001-01-17
Prior application date removed - consult PALM or file wrapper
SOFTWARE: PACE IN NOS: 10231
SOFTWARE: PACENTIN Ver. 2.0
SEQ ID NOS: 1531
FastSEQ for Windows Version 4.0
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OTHER INFORMATION: b=g or c or t/u
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OTHER INFORMATION: k=g or t/u
NAME/KEY: misc_feature
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82.8%;
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OTHER INFORMATION: w=a or t/u
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OTHER INFORMATION: y=t/u or
NAME/KEY: misc_feature
LOCATION: (1)...(1531)
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OTHER INFORMATION: s=g or c
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OTHER INFORMATION: m=a or
NAME/KEY: misc_feature
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Best Local Similarity 82.8
Matches 149; Conservative
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OTHER INFORMATION: d=a or
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OTHER INFORMATION: v=a
                                                                                             TYPE: DNA
ORGANISM: Homo sapiens
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OTHER INFORMATION: h=a
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LOCATION: (1)...(1531)
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                                                                          Length 4045;
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TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC006
CURRENT APPLICATION NUMBER: US/09/764,891
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper
NUMBER OF SQL ID NOS: 10231
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 8119
LENGTH: 4045
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Pred. No. 9.9e-24;
0; Mismatches 57
                                                                                        Pred. No. 9.9e-24
                                                                                                        0; Mismatches
                                                                          24.0%; Score 119.8; 73.0%; Pred. No. 9.9e
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Publication No. US20030077808A1
GENERAL INFORMATION:
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US-08-927-939-78/c
; Sequence 78, Application US/08927939
; Patent No. US20010006640A1
; GENERAL INFORMATION:
; APPLICANT: Grainger, David J.
; APPLICANT: Tatalick, Lauen Marie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 73.0%;
Matches 154; Conservative
                                                                     Query Match
Best Local Similarity 73.0
Matches 154; Conservative
            TYPE: DNA
ORGANISM: Homo sapiens
US-09-764-891-8718
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; ORGANISM: Homo sapiens
US-09-764-891-8719
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US-09-764-891-8719
LENGTH: 4045
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GENERAL INFORMATION:
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TITLE OF INVENTION:
FILE REFERENCE: 689290-77
CURRENT FILING DATE: 2002-05-02
FRICK APPLICATION NUMBER: US/60/233,133
FRIOR FILING DATE: 2000-09-18
FRIOR APPLICATION NUMBER: US/60/234,009
FRIOR FILING DATE: 2000-09-20
FRIOR FILING DATE: 2000-09-20
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TITLE OF INVENTION: Compounds and methods to inhibit or TITLE OF INVENTION: augment an inflammatory response. FILE REPERENCE: 295.025031 CURRENT APPLICATION NUMBER: US/08/927,939 CURRENT FILING DATE: 1997-09-11 NUMBER OF SEQ ID NOS: 83 SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 78
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Pred. No. 5.6e-24;
0; Mismatches 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 8;
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Pred. No. 5.6e-24;
0; Mismatches 29
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; Patent No. US20020165180A1
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Best Local Similarity 82.5%;
Matches 137; Conservative (
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Best Local Similarity 82.5%;
Matches 137; Conservative
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ORGANISM: Homo sapiens
US-09-954-531-146
                                                                                                                                                                                                                                                                   ORGANISM: Homo sapiens
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; NAME/KEY: CDS
; LOCATION: (27)...(299)
US-08-927-939-78
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US-09-954-531-146/c
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ORGANISM: human
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SERVICANT: MERKULOW, Gennady V. et al
TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: CLOO1012CON
CURRENT APPLICATION NUMBER: US/10/237,859
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastseQ for Windows Version 4.0
SEQ ID NO 3
LENGTH 73467
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Patent No. US20020076774A1

GENERAL INFORMATION:
TITLE OF INVENTION: ISOLATED HUMAN DRUG-METABOLIZING
TITLE OF INVENTION: BROTEINS, WUCLEIC ACID MOLECULES ENCODING HUMAN
TITLE OF INVENTION: AND USES THEREOF
TITLE OF INVENTION: AND USES THEREOF
TITLE OF INVENTION: AND USES THEREOF
CURRENT APPLICATION NUMBER: US/09/748,127

CURRENT PILING DATE: 2001-06-11
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH 17752
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299 GCCTCAGCCTCCCAAGTAGCTGGGACTACAAGCTCGGGACACCACG 344
                                      647 gectreagecreegagrageriggaactracaggegegegetacaeg 602
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; NAME/KEY: misc_feature
; LOCATION: (1)...(73467)
; OTHER INFORMATION: n = A,T,C or G
US-10-237-859-3
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; LOCATION: (1)...(17752)
; OTHER INFORMATION: n = A,T,C or G
US-09-748-127-3
                                                                                                                                                , Sequence 3, Application US/10237859
; Publication No. US20030022309A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Human
                                                                                                                            US-10-237-859-3/c
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US-09-748-127-3
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23.7%; Score 118.4; DB 10; Length 17752;

Query Match

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                                                                                                FTGAGACAGGGTCTCGAGGTGTCACCC 230
                                                                                                                                                                                                                                231 AGGCTGGAGTGCAGTGGCGCGATTTCGACTCACCGCAACCTCCGCCTCCGCGCTTAAGCG 290
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                                  0; Gaps
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23.7%; Score 118.4; DB 10; Length 465237;
Best Local Similarity 67.5%; Pred. No. 3.6e-22;
Matches 181; Conservative 0; Mismatches 86; Indels 1; G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FALENT NO. USZUGAZUIZJUSSAI

GENERAL INTORMATION: Estrogen receptor alpha variants and TITLE OF INVENTION: Betrogen receptor alpha variants and TITLE OF INVENTION: Betrogen receptor alpha variants and TITLE OF INVENTION: methods of detection thereof FILE REFERENCE: CLORO0258C14

CURRENT APPLICATION NUMBER: US/09/933,267A

CURRENT FILING DATE: 2000-08-21

PRIOR APPLICATION NUMBER: 60/160666

PRIOR PILING DATE: 2000-02-22

PRIOR PILING DATE: 2000-102-26

PRIOR PAPLICATION NUMBER: 09/692414

PRIOR PILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 09/768184

PRIOR PILING DATE: 2001-01-24

PRIOR PILING DATE: 2001-03-13

PRIOR PILING DATE: 2001-04-05

NUMBER OF SEQ ID NOS: 2

SOFTWARE: PASTSEQ for Windows Version 4.0
                               Indels
   Pred. No. 5.7e-23;
0; Mismatches 41;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1, Application US/09933267A Patent No. US20020123095A1
                                                                                                   171 AACACTACAATTTTTTTTTTTTTTTTT
Best Local Similarity 77.7%;
Matches 143; Conservative
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Db 11696 CAGGCGCCCGCCACCACGCCCAGCTAAT 11669

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                                           Sequence 3707, Application US/09764877
Fatent No. US20020147140A1
GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION:
PLE REFERENCE: PC005
CURRENT APPLICATION NUMBER: US/09/764,877
CURRENT FILING DATE: 2001-01-17
Prior application data removed - refer to PALM or file wrapper
NUMBER OF SEQ ID NOS: 4031
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 3707
LENTH: 5159
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; Publication No. US20030077808A1
; GENERAL INFORMATION:
    APPLICANT: Rosen et al.
    TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
    FILE REFERENCE: PC006
; CURRENT APPLICATION NUMBER: US/09/764,891
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 10231
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8002
; LENGTH: 6834
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Pred. No. 3.2e-23;
0; Mismatches 28; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 82.8%;
Matches 135; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
CORGANISM: Homo sapiens
US-09-764-877-3707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-891-8002
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US-09-764-891-8002
RESULT 14
US-09-764-877-3707
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(cgn2_6/ptodata/2/ina/5A_COMB.seq:*
/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
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US-09-173-914-6
US-08-724-394A-21
US-08-724-394A-22
US-08-757-223-7
US-09-757-223-7
US-09-797-906-3
US-08-759-839-5
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US-09-210-748A-3
US-09-81-896-3
US-09-797-906-3
US-09-732-025-3
US-09-734-675-3
US-09-851-896-3
US-09-851-896-3
US-08-310-356-36
PCT-US92-06300-1
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                                 version :
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                             nucleic search, using sw model
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                                 GenCore (c) 1993
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length: 2000000000
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Sequence Sequence

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| Fatelin No. bi334903
| GRUERAL INFORMATION:
| APPLICANT: Tartigian, Sean V.
| APPLICANT: Tartigian, Sean V.
| APPLICANT: Simard, Jacques
| APPLICANT: Sommens, Johanna M.
| APPLICANT: Myriad Genetics, Inc.
| APPLICANT: Myriad Genetics, Inc.
| TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility
| TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility
| TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes
| CURRENT APPLICATION NUMBER: US/09/564,805
| CURRENT FILING DATE: 12000-05-05
| PRIOR APPLICATION NUMBER: US 60/107,468
| PRIOR APPLICATION NUMBER: 09/434,382
| PRIOR FILING DATE: 1999-11-05
| NUMBER OF SEQ ID NOS: 240
                                                                                                                                                                       Sequence 1, Appli
Sequence 5, Appli
Sequence 3, Appli
Sequence 12, Appl
Sequence 3, Appli
Sequence 3, Appli
Sequence 629, App
Sequence 629, App
Sequence 630, App
Sequence 5, Appli
Sequence 1, Appli
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Sequence 27, Appl
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Sequence 19, Appli
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OTHER INFORMATION: exon 19: 23045-23154; exon 20: 23795-23895; exon OTHER INFORMATION: exon 19: 23045-23154; exon 22: 24354-24432; exon 23: OTHER INFORMATION: 25026-25170; exon 24: 25912-26036; polyadenylation OTHER INFORMATION: signal: 26447-26452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION: s at positions 826 and 23180 is G or C; y at INFORMATION: positions 1914, 5558, 7165, 16431, 1857 and 20486 INFORMATION: is C or T; n at position 13128 is t or tgat; r at INFORMATION: positions 22211 and 23879 is A or G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MAMB/KEY: misc feature
LOCATION: (910)...(13104)
OTHER INFORMATION: exon 1: 910-1154; exon 2: 1736-1786; exon 3:
OTHER INFORMATION: exon 6: 5582-5560; exon 7: 7075-7194; exon 8:
OTHER INFORMATION: exon 6: 5582-5560; exon 7: 7075-7194; exon 8:
OTHER INFORMATION: 8186-8244; exon 9: 12878-12936; exon 10:
NAME/KEY: misc feature
LOCATION: (13756)..(22317)
OTHER INFORMATION: exon 11: 13756-13868; exon 12: 15283-15378; exon OTHER INFORMATION: 13: 16278-16416; exon 14: 16498-16583; exon 15: OTHER INFORMATION: 13: 16278-16416; exon 16: 20349-22945; exon 17:
US-09-630-706-10
US-09-496-694B-3
US-09-070-294-27
US-09-070-294-3
US-09-345-8B-3
US-08-35-048-5
US-08-965-048-6
US-09-741-154-3
US-09-0741-154-3
US-09-0741-156-3
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; Sequence 28, Application US/09564805
; Patent No. 6333403
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ORGANISM: Homo sapiens
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LOCATION: (826)..(23
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NAME/KEY: misc_feature
LOCATION: (1)...(84495)
OTHER INFORMATION: n = A,T,C or
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ORGANISM: Human
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LENGTH: 84495
                                                                                                                                                                                                                                                  US-09-851-896-3/c
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                                                                                                                                                                                                                                                 241 GCAGTGGCGCGATTTCGACTCACCGCAACCTCCGCCTTCGCGCGTTTCTCCTGC 300
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                                                                                                                                                                           61 TTTACACATAAGAAAGCTGAGGCTCTGAGAGGTCAAGATCACGCAGCTAACAAATGAGCC 120
                                                                                                     1 TATCAGGTGACTGAATTCTATATTCTGAAGTAGGAGATACTGTTATTGCTGTTATTACAT 60
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                                                                                                                                                                                                                                                                                                                     TTTTTGTTTTGTTTTGTTTTTGAGACAGGGTCTCGAGGTGTCACCCAGGCTGGAGT
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24.1%; Score 120.4; DB 4; Length 7680;
Best Local Similarity 74.3%; Pred. No. 8.1e-25;
Matches 165; Conservative 0; Mismatches 56; Indels 1;
                                 100.0%; Score 500; DB 4; Length 26664; 100.0%; Pred. No. 8.5e-133;
                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Vicinity Bert
APPLICANT: Kinzler, Kenneth
TITLE OF INVENTION: 14-3-3 SIGMA ARREST THE CELL CYCLE
TITLE OF INVENTION: 14-3-3 SIGMA ARREST THE CELL CYCLE
FILE REPERENCE: 1107.77810
CURRENT FILING DATE: 1998-12-15
PRIOR APPLICATION NUMBER: 60/069,416
PRIOR FILING DATE: 1997-12-18
NUMBER OF SEQ ID NOS: 18
SOFTWARE: FastSEQ for Windows-Version 3.0
SEQ ID NO 3
LENGTH: 7680
                                                                     ;
0
                                                                    0; Mismatches
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Patent No. 6335156
GENERAL INFORMATION:
APPLICANT: Hermeking, Heiko
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAGCTCTGAGGGACTGACGT 500
                                                                    Matches 500; Conservative
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                                                   Similarity
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US-09-210-748A-3
US-09-564-805-28
                                  Query Match
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APPLICANT: C. Frank Bennett
APPLICANT: Susan M. Freier
APPLICANT: Andrew T. Watt
TILLE OF INVENTION: ANTISENSE MODULATION OF PHOSPHOLIPASE A2, GROUP VI (CA2+-INDEPEND
TILLE OF INVENTION: EXPRESSION
FILE REFERENCE: RTS-0220
CURRENT APPLICATION NUMBER: US/09/851,896
CURRENT FILING DATE: 2001-05-08
NUMBER OF SEQ ID NOS: 89
SEQ ID NO 3
LENGHAT 70000
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Patent No. 6329188
GENERAL INFORMATION:
APPLICANT: Zianghe YAN, Karen A. KETCHUM, Valentina DIFRANCESCO, Ellen M. BEASLEY
TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,
TITLE OF INVENTION: USES THEREOF
TITLE OF INVENTION: USES THEREOF
TITLE OF INVENTION: USES THEREOF
CURRENT APPLICATION NUMBER: US/09/797,906
CURRENT FILING DATE: 2001-03-05
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PASKESQ for Windows Version 4.0
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5946 rrrrrrgrrgrrrrrgrrrraagacgaagrcrrgcrcracccaggcrgaagga 6005
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                                                                                                                                            GTGGCGCGATTTCGACTCACCGCAACCTCCGCCT-CCGCGCTTAAGCGATTCTCCTGCCT
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Pred. No. 3.3e-24;
0; Mismatches 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 3, Application US/09851896; Patent No. 6410325; GENERAL INFORMATION:
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Best Local Similarity 80.5
Matches 140; Conservative
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ORGANISM: Human
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US-09-734-673-3
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APPLICANT: WEI, MING-Hui et al
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
TITLE OF INVENTION: THEREOF
FILE REPERENCE: CLOOIO11
CURRENT APPLICANDIO11
CURRENT APPLICANDIO11
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PaetSEQ for Windows Version 4.0
SEQ ID NO 3:
LENGTH: 8285
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                                                                                                                                        146 TCTATTCTTGCTTTTCCAAAAACACTACAATTTTTGTTTTGTTTTGTTTT
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                               Length 84495
                                                        Indels
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                            DB 4;
                                                         89;
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                          Score 115.6; DB 4
Pred. No. 4.9e-23;
0; Mismatches 89
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LOCATION: (1)...(8285)
OTHER INFORMATION: n = A,T,C or G
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Patent No. 6416990
                          Query Match 23.1%;
Best Local Similarity 66.7%;
Matches 180; Conservative (
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US-09-732-025-3
US-09-797-906-3
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Sequence 3, Application US/09739455

Patent No. 6413756

GENERAL INFORMATION:
APPLICANT: YAN, Chunhua et al
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
TITLE OF INVENTION: THERE WE SUCCESS
TITLE OF INVENTION: THERE WE SUCESS
TITLE OF INVENTION: THERE WE SUCCESS
TITLE OF INVENTION: UNMERR: US/09/739,455
CURRENT PALLICATION NUMBER: US/09/739,455
CURRENT FILING DATE: 2000-12-19
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO : SEQ ID NOS: 23
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TITLE OF INVENTION: ISOLATED HUMAN KINASE PROFEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: CLOO1020
CURRENT APPLICATION NUMBER: US/09/734,673
CURRENT APPLICATION NUMBER: LOO-12-13
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FASELSEQ for Windows Version 4.0
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Best Local Similarity 67.3%; Pred. No. 5.3e-23;
Matches 177; Conservative 0; Mismatches 85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 23.1%; Score 115.4; DB 4 Best Local Similarity 74.1%; Pred. No. 2.6e-23; Matches 146; Conservative 0; Mismatches 51
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LOCATION: (1)...(11827)
OTHER INFORMATION: n = A,T,C or G
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; OTHER INFORMATION: n = A,T,C or G
US-09-734-673-3
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Patent No. 6410294
GENERAL INFORMATION:
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ZIP: 19426

ZIP: 19426

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Macintosh
OPERATING SYSTEM: Macintosh System 7.0
SOFTWARE: Microsoft Word Version 5.0 (PatentIn)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/310,356
  ADDRESSEE: Rhone-Poulenc Rorer Legal Department
STREET: 500 Arcola Road
CITY: Collegeville
                                                                                                                                                                                                                                                                                  APPLICATION: 800
CLASSIFICATION: 800
CLASSIFICATION DATA:
APPLICATION NUMBER: US/07/737,853
FILING DATE: 31-JUL-1991
ATTORNEY/AGENT INFORMATION:
NAME: Goodman, Rosanne
REGISTRATION NUMBER: 32,534
REFERENCE/DOCKET NUMBER: A0856
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 454-3801
TELEPHONE: (215) 454-3808
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
TENGTH: 19011 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: intron
LOCATION: 1855..2563
OTHER INFORMATION: /number= 1
OTHER INFORMATION: /label= intron1
OTHER INFORMATION: /citation= ([1])
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LOCATION: 6802..6934
OTHER INFORMATION: /number= 5
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TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FBATURE:
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LOCATION: 2622..4075
OTHER INFORMATION: /number=
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OTHER INFORMATION: /number=
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LOCATION: 6041..6252
OTHER INFORMATION: /number=
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NAME/KEY: exon
LOCATION: 4076..4208
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                                                                                             COUNTRY:
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US-09-81-896-3
US-09-81-896-3
Sequence 3, Application US/09851896
Patent No. 6410325
GENERAL INFORMATION:
PAPLICANT: C. Frank Bennett
APPLICANT: Susan M. Freier
APPLICANT: Andrew T. Watt
TITLE OF INVENTION: EXPRESSION
FILE REFERENCE: RTS-0220
CURRENT APPLICATION UNMBER: US/09/851,896
CURRENT FILING DATE: 2001-05-08
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                                                                                                                                                                                                                                                                                                     33002 CCTCCCAAGTAGCTGGGATTACAGGCATGTCCACCATGCCTAGCTGATTTTGTGTTTTT 33061
                                                                                                                                                                  247 GCGCGATTTCGACTCACCGCAACCTCCGCCT-CCGCGCTTAAGCGATTCTCCTGCCTCAG 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         214 GTCTCGAGGTGTCACCCAGGCTGGAGTGCAGTGGCGGGATTTCGACTCACCGCAACCTCC 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  274 GCCTCCGCGCTT-AAGCGATTCTCCTGCCTCAGCCTCCCAAGTAGCTGGGACTACAAGCT 332
                                                                                                                                                                                                                                                          306 CCTCCCCAAGTAGCTGGGACTACAAGCTCGGGACACCACGTAAAAATGATCAAGTTCTAAC 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               154 TGCTTTTCTTTTCCAAAAAACACTACAATTTTTTGTTTTTGTTTTTGTTTTTGAGACAGG 213
                                                                       187 TTTTGTTTTGTTTTGAGACAGGGTCTCGAGGTGTCACCCCAGGCTGGAGTGCAGTG
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Live 0; Mismatches 42; Indels
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Sequence 36, Application US/08310356

Patent No. 5648243

GENERAL INFORMATION:
APPLICANT: Hurwitz, David R
APPLICANT: Nathan, Margret
APPLICANT: Shani, Moshe
TITLE OF INVENTION: Transgenic Protein Production
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                             33062 AATAGAGATGAGGTTTCACCATG 33084
                                                                                                                                                                                                                                                                                                                                                  366 ATGTATGCATACGAATTACAATG 388
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Best Local Similarity 77.6
Matches 149; Conservative
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          333 CGGGACACCACG 344
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LENGTH: 70000
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FEATURE:

NAME/KEY: intron

LOCATION: 6935..758

CHER INFORMATION: /number= 6

FEATURE:

NAME/KEY: mitton

LOCATION: 7759..7866

COTHER INFORMATION: /number= 6

FEATURE:

NAME/KEY: intron

LOCATION: 9574..943

COTHER INFORMATION: /number= 7

FEATURE:

NAME/KEY: intron

LOCATION: 9574..10866

COTHER INFORMATION: /number= 7

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NAME/KEY: intron

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COTHER INFORMATION: /number= 9

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NAME/KEY: intron

LOCATION: 12644..13701

COTHER INFORMATION: /number= 10

FEATURE:

NAME/KEY: intron

LOCATION: 13702..13799

COTHER INFORMATION: /number= 11

FEATURE:

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LOCATION: 13600..14976

COTHER INFORMATION: /number= 11

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LOCATION: 15116..15533

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LOCATION: 15534..15757

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LOCATION: 15534..15757

COTHER INFORMATION: /number= 13

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NAME/KEY: intron

LOCATION: 15534..15757

COTHER INFORMATION: /number= 13

FEATURE:

NAME/KEY: intron

LOCATION: 15534..15757

COTHER INFORMATION: /number= 13

FEATURE:

NAME/KEY: intron

LOCATION: 15769..17082

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FEATURE:

NAME/KEY: intron

LOCATION: 15769..17082

LOCATION: 15769..17082

LOCATION: 15769..17082

LOCATION: 17083..1764

COTHER INFORMATION: /number= 13

FEATURE:

NAME/KEY: intron

LOCATION: 17083..1764

COTHER INFORMATION: /number= 13

FEATURE:

NAME/KEY: intron

LOCATION: 17083..1764

COTHER INFORMATION: /number= 13

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LOCATION: 17083..1764

COTHER INFORMATION: /number= 13

FEATURE:

NAME/KEY: intron

LOCATION: 17083..1764

COTHER INFORMATION: /number= 13

FEATURE:

NAME/KEY: intron

LOCATION: 17083
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3098 GCGCAATCTCGGCTCACTGCAAACTCCGCGTTCACGCCATTCTCCTGCCTCAGC 3157
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   187 ITTTGTTTTGTTTTTGAGACAGGGTCTCGAGGTGTCACCCAGGCTGGAGTGCAGTG 246
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                                                                                                                           CCATION: 1020 (1776..1854, 2564..2621, 4076..4208, LOCATION: 5011(1776..1854, 2564..2621, 4076..4208, LOCATION: 6041..6252, 6802..6934, 7759..7856, 9444..9573, LOCATION: 10867..11081, 12613, 13702..13799, LOCATION: 17697..15115, 15534..15757, 16950..17082, LOCATION: 17697..17741, OTHER INFORMATION: /product= "human serum albumin" OTHER INFORMATION: /cication= ([1])

FEATURE:
NAME/KEY: exon
LOCATION: 18535.18697
OTHER INFORMATION: /number= 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AUTHORS: Dugaiczyk, A TITLE: MOLECULAR STRUCTURE OF THE HUMAN ALBUMIN TITLE: GNE IS REVEALED BY NUCLEOTIDE SEQUENCE WITHIN TITLE: q11-22 OF CHROMOSOME 4
JOURNAL: J. Biol. Chem.
VOLUME: 221
PAGES: 6747-6757
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PCT-US92-06300-1
SGQUENCE 1, Application PC/TUS9206300
GENERAL INFORMATION:
APPLICANT: Hurwitz, David R
APPLICANT: Nathan, Margret
APPLICANT: Shani, Moshe
TTLE OF INVENTION: Transgenic Protein Production
NUMBER OF SEQUENCES: 1
CORRESPONDENCE S. 1
CORRESPONDENCE ADDRESSE:
ADDRESSEE: Rhone-Poulenc Rorer, Inc.
STREET: 500 Virginia Ave., Bldg. 3A
CITY: Ft. Washington
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3158 CTCCCGAGTAGCTGGGACTACAGGCGCCCGCCATCACG 3195
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; PAGES: 6747-6757
; DATE: 1986
; RELEVANT RESIDUES IN SEQ ID NO:
US-08-310-356-36
NAME/KEY: intron
LOCATION: 17765..18534
OTHER INFORMATION: /number= 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
NAME/KEY: 5'UTR
LOCATION: 1737...175
PUBLICATION: 1737...175
PUBLICATION: REACHER, DE AUTHORS: Ruffner, D E AUTHORS: Rung, W-J
AUTHORS: Hawkins, J W
AUTHORS: Beattie, W G
AUTHORS: Beattie, W G
AUTHORS: Beattie, W G
AUTHORS: Dugaiczyk, A
                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
NAME/KEY: 3'UTR
LOCATION: 17742..18697
                                                                                                             NAME/KEY:
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1299 Pennsylvania Avenue, N.W
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SEQUENCE CHARACTERISTICS:
LENGTH: 2099 base pairs
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Best Local Similarity 83.6
Matches 138; Conservative
                                                                                                                                          Diskette
                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: sing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear MOLECULE TYPE: CDNA
STREET: 1255
                                                                        COUNTRY: USA
ZIP: 20004-2402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 14636
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3593 TTAATTTTTTTTTTTTTAAGACAGGGTCTCGCTCTGTCGCCCAGGCTGGAGTGCAGTG 3652
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Nguyen, Thai D.
APPLICANT: Nguyen, Thai D.
APPLICANT: Polansky, Jon R.
TITLE OF INVENTION: METHODS FOR THE DIAGNOSIS,
TITLE OF INVENTION: RELATED DISEASES
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Howrey & Simon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IS REVEALED BY NUCLEOTIDE SEQUENCE WITHIN Q11-22 OF CHROMOSOME 4 : J. Biol. Chem.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 22.3%; Score 111.6; DB 5; Length 1 Best Local Similarity 81.6%; Pred. No. 3.8e-22; Matches 129; Conservative 0; Mismatches 29; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1: FROM 1 TO 19002
           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/06300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3713 CTCCCGAGTAGCTGGGACTACAGGCGCCCCCATCACG 3750
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                                                                                                                                                                                                                                                                        A0856-US
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JOURNAL: J. Biol. Chem.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DATE: 1986
RELEVANT RESIDUES IN SEQ ID NO:
PCT-US92-06300-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 11
18-08-938-669A-5
Sequence 5, Application US/08938669A
; Patent No. 6171788
                                                                                                                                                      FILING DATE: 19920730
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: GOOGMEN, ROSEATHE
REGISTRATION NUMBER: 52,534
REFERENCE/DOCKET NUMBER: 40856
TELEPAN: (215) 962-4130
TELEPAN: (215) 962-4130
TELEPAN: (215) 962-4130
TELEPAN: (215) 962-4107
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 19557 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ANTI-SENSE:

ANTI-SENSE:

PUBLICATION:

AUTHORS: Minghetti, P P
AUTHORS: Ruffner, D B
AUTHORS: Kuang, W.-J.

AUTHORS: Hawkins, J W
AUTHORS: Hawkins, J W
AUTHORS: Beattie, W G
AUTHORS: Beattie, M G
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GENERAL INFORMATION:
APPLICANT: Hendrickson, Eric
TITLE OF INVENTION: A No. 6171857el Leucine Zipper, KARP-1 and
TITLE OF INVENTION: A No. 6171857el Leucine Zipper, KARP-1 and
TITLE OF INVENTION: Methods of Regulating DNA Dependent Protein Kinase Activity
TITLE OF INVENTION: WORTHOUSER: US/09/173,914
CURRENT FELING DATE: 1998-10-16
EARLIER APPLICATION NUMBER: 60/064,557
EARLIER FILING DATE: 1997-10-17
NUMBER OF SEQ ID NOS: 35
SOFFWARE: FastSEQ for Windows Version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22.3%; Score 111.4; DB 4;
83.6%; Pred. No. 1.8e-22;
live 0; Mismatches 26;
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
CUPTWARE: PastsED for Windows Version 2.0
SUGRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/938,669A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              07425-0034
                                                                                                                                                                                                                                                                                                                                             FILING DATE:
CLASSIFICATION: 435
PRICAR APPLICATION DATE:
APPLICATION DATE:
FILING DATE: 28-JAN-1997
ATTORNEY FAGENT INFORMATION:
NAME: Mendelson, Blioc
REGISTRATION NUMBER: P-42,878
TELECOMMUNICATION INFORMATION:
TELEFHONE: 202 383-6610
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Patent No. 6171857
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Db 148134 CCTCAGCCTCCCGAGTAGCTGGGACTACAGGCGCCCACCATCACGCCCAGCTAATTATT 148193
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                                                                                    Db 148074 GCCATGGCGCGATCTCGGCTCACTGCAAGCTCCGCCTCCCGGGTTCACGCCATTCTCCTG
                                                                                                                                             300 CCTCAGCCTCCCAAGTAGCTGGGACTACAAGCTCGGGACACCACGTAAAAATGATCAAGT
                                                    241 GCAGTGGCGCGATTTCGACTCACCGCAACCTCCGCCT-CCGCGCTTAAGCGATTCTCCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Krommal, Gregory S.
APPLICANT: Lauer, Peter M.
APPLICANT: Lauer, Peter M.
APPLICANT: Tandry, David A.
APPLICANT: Thomas, Winston
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Wolff, Roger K.
TITLE OF INVENTION: Megabase Transcript Map: No. 587
TITLE OF INVENTION: Sequences and Antibodies Thereto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: BATEMIN PC-DOS/MS-DOS
SOFTWARE: PATEMIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/724,394A
FILING DATE: 01-0CT-1996
CLASSIFICATION: 536
ATTONNEY/AGENT INPORMATION:
NAME: Fitts, Renee A.
REGISTRATION NUMBER: 35,136
REGISTRATION NUMBER: 35,136
REGISTRATION NUMBER: 017957-000100
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
                                                                                                                                                                                                                                                                               Db 148194 İGTATTITIAGİAGACGGGTITCAİCGIGITAA 148229
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Pred. No. 1.3e-21;
0; Mismatches 58
                                                                                                                                                                                                                                      360 TCTAACATGTATGCATACGAATTACAATGGAAATAA 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "HLA-H.CONTIG"
                                                                                                                                                                                                                                                                                                                                                                                           Sequence 21, Application US/08724394A Patent No. 5872237 GENERAL INFORMATION: APPLICANT: Feder, John N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 415-576-0300
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 246240 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SS: not relevant
not relevant
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72.7%;
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LOCATION: 1..246240
OTHER INFORMATION: /not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 94111-3334
COMPUTER READABLE FORM:
MEDIUM TYPE: Flore:
COMPUTER: TP'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid STRANDEDNESS: not
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
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                                                                                                                12228 TITITITITITITITITITITITITITIGAGACGGAGTCTCGCTCTGTCGCCCAGGCTGGAGT 12287
                                                                                                                                                                                                         12288 GCAGTGGCGGGATCTCGGCTCACTGCAAGCTCCGCCTCCCGGGTTCACGCCATTCTCCTG 12347
                                                                        GTTTTGAGACAGGGTCTCGAGGTGTCACCCAGGCTGGAGT 240
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                          Gaps
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                                                                                                                                                              241 GCAGTGGCGCGATTTCGACTCACCGCAACCTCCGCCT-CCGCGCTTAAGCGATTCTCCTG
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                          1;
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                          Indels
                                                                                                                                                                                                                                                                                 12348 CCTCAGCCTCCCAAGTAGCTGGGACTACAGGCGCCCGCCACTACG 12392
                                                                                                                                                                                                                                                       300 CCTCAGCCTCCCAAGTAGCTGGGACTACAAGCTCGGGACACCACG 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Megabase Transcript Map: No. 58 TITLE OF INVENTION: Sequences and Antibodies Thereto
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MEDIUM TYPE: Floppy disk

WEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/724,394A
FILING DATE: 01-OCT-1996
CLASSIFICATION: 53 6
ATTORNEY/AGBNT INFORMATION:
NAME: Fitts, Renee A.
REFERENCE/DOCKET NUMBER: 35,136
REFERENCE/DOCKET NUMBER: 017957-000100
TELECOMMUNICATION INFORMATION:
TELEDEHONE: 415-576.0200
Pred. No. 3.8e-22;
0; Mismatches 26;
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ADDRESSEE: TOWNSEND and TOWNSEND and CREW
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ) NAME/KEY: misc_feature

) LOCATION: 1..246240

) OTHER INFEMATION: /note= "HLA-H.CONTIG"

US-08-724-3848-20
                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 20, Application US/08724394A
Patent No. 5872237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kronmal, Gregory S.
Lauer, Peter M.
Ruddy, David A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : Thomas, Winston
: Tsuchihashi, Zenta
: Wolff, Roger K.
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STRANDEDNESS: not relevant
TOPOLOGY: not relevant
DLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 415-576-0300
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 246240 base pairs
83.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         John N.
                          Matches 138; Conservative
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Best Local Similarity
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US-08-724-394A-20
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STATE: CA
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
APPLICANT:
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APPLICANT:
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Db 148014 Thaittitititititititititagaaaciccccrcigicaacccagacicgaan 148073
Db 148074 GCCATGGCGCGATCTCGGCTCACTGCAAGCTCCGCCTCCCGCGTTCACGCCATCTCCTG 148133
                                                                                                    Db 148134 CCTCAGCCTCCCGAGTAGCTGGGACTACAGGCGCCCACCATCACGCCCAGCTAATTATT 148193
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                                                                      CCTCAGCCTCCCAAGTAGCTGGGACTACAAGCTCGGGACACCACGTAAAAATGATCAAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 22.2%; Score 111.2; DB 2; Length 246240; Best Local Similarity 72.7%; Pred. No. 1.3e-21; Matches 157; Conservative 0; Mismatches 58; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          No. 5872237el
                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Feder, John N.
APPLICANT: Fromal, Gregory S.
APPLICANT: Rundy, David A.
APPLICANT: Thomas, Winston
APPLICANT: Thomas, Winston
APPLICANT: Wolff, Roger K.
ITLE OF INVENTION: Megabase Transcript Map: No. 587223
TITLE OF INVENTION: Sequences and Antibodies Thereto
NUMBER OF SUGUENCES: 31
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/724,394A
FILING DATE: 01-OCT-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Filts, Renee A.
REGISTRATION NUMBER: 35,136
REFERENCE/DOCKET NUMBER: 017957-000100
TELEPHONE: 415-576-020
TELEFAX: 415-576-020
TELEFAX: 415-576-020
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 246240 base pairs
                                                                                                                                                                                                                           Db 148194 İGTATTITIAGİAGAĞĞĞĞĞTITCAİCĞIĞITAA 148229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOWNSEND and TOWNSEND and CREW LLP
                                                                                                                                                                          360 TCTAACATGTATGCATACGAATTACAATGGAAATAA 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc_feature
| JOCATION: 1..246240
| OTHER INFORMATION: /note= "HLA-H.CONTIG"
US-08-724-394A-22
                                                                                                                                                                                                                                                                                                                                                           Sequence 22, Application US/08724394A Patent No. 5872237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid STRNDEDNESS: not relevant TOPOLOGY: not relevant MOLECULE TYPE: CDNA
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US-08-724-394A-22
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        Qy
        241 GCAGTGGCGCGATTTCGACTCACCGCAACCTCCGCGCTTAAGCGATTCTCCTG
        299

        Qy
        241 GCAGTGGCGCGTTTCACGCTCCCGCCTCCCGCGTTCTCCTG
        299

        Db
        148074 GCCATGGCGCGTCTCGGCTCCCGCGTTCCTCTG
        148133

        Qy
        300 CCTCAGCCTCCCAAGTGCTGGACTACAAGCTCGGGACACCACGTAAATGATCAAGT
        359

        Db
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Search completed: May 17, 2003, 16:46:58 Job time : 416.134 secs

May 17, 2003, 15:56:54 ; Search time 2075.34 Seconds (without alignments) 11232.524 Million cell updates/sec OM nucleic - nucleic search, using sw model Run on:

US-09-434-382-28_COPY_21800_22600 Perfect score: Title:

1 agtgcctgtcctggtattt......agcggaagctttgaccggat 801 IDENTITY NUC Gapop 10.0 , Gapext 1.0 Scoring table: Sequence:

2054640 segs, 14551402878 residues Searched: Total number of hits satisfying chosen parameters:

4109280

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

GenEmbl:* Database :

gb htg: gb htg: gb loon: gb oon: gb oon: gb bh: gb bh: gb bh: gb bh: gb vi: gb vi: em fun: em fun: em fun: em oon: em oon:

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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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AC005277 118788 bp DNA linear PRI 23-JUL-1998 Homo sapiens chromosome 17, clone hRPK.597_M_12, complete sequence. AC005277 AC005277.1 GI:3337311 RESULT 1
ACO05277
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

Homo sapiens. Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 118788)

Birren, B., Fasman, K., Linton, L., Nusbaum, C. and Lander, E. Homo sapiens chromosome 17, clone hRPK.597_M_12

Unpublished REFERENCE AUTHORS TITLE JOURNAL

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15683. 15759
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20263. .2nff
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ement (2002)
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             Baker, B. Fagman, K., Linton, L., Nusbaum, C., Lander, E., Allen, N., Baker, J., Baldwin, J., Barna, N., Beckerly, R., Benn, J., Boatin, C., Bouwell, C., Brown, A., Castle, A., Cerry, J., Cooke, P., Depayre, E., Devon, K., Dewar, K., Donelan, L., Etemadi, S., Ferreira, P., FitzHugh, W., Forrest, C., Funke, R., Gage, D., Gardyna, S., Gensheimer, S., Geraglery, K., Gilmartin, T., Grant, G., Hagos, B., Harris, K., Horton, L., Howland, J.C., Hui, L., Jacotot, L., Kann, L., Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., Melharim, J., Molla, M., Morris, W., Morrow, J., Mychaleckyj, J., Nachman, A., Nahf, R., Naylor, J., Nioff, M., O'Connor, T., Pavlin, B., Peterson, K., Riley, R., Roberts, D., Rossello, R., Roy, A., Stange-Thomann, N., Stilwell, J., Stojanovic, N., Stone, C., Strickland, C., Subramanian, A., Torruella-Miller, I., Vassiliev, H., Vo, A., Wagner, A., Wang, B., Wheeler, J., Wu, Y., Ye, W.J., Zhao, J. and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                      Submitted (10-JUL-1998) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
3 (Dases I to 118708)
Baren, D. 18708
Baker, J., Baldwin, J., Barna, N., Beckerly, R., Benn, J., Boatin, C., Baker, J., Baldwin, J., Berkerly, R., Benn, J., Boatin, C., Boutwell, C., Brown, A., Castle, A., Cerny, J., Cooke, P., Depayre, E., Devon, K., Dewar, K., Donlan, L., Etemadi, S., Ferreira, P., FitzHugh, W., Forrest, C., Funke, R., Gage, D., Gardyna, S., Genshehamer, S., Geragery, K., Gilmartin, T., Garnt, G., Hagos, B., Harris, K., Horton, L., Howland, J.C., Hui, L., Jacotot, L., Kann, L., Macdonald, P., Marquis, N., Morris, W., Morrow, J., Mychaleckyj, J., Nachman, A., Nahl, R., Naylor, J., Niloff, M., O'Connor, T., Pavlin, B., Peterson, K., Riley, R., Roberts, D., Rossello, R., Roy, A., Shyam, R., Stange-Thomann, M., Stilwell, J., Stojanovic, N., Stone, C., Subramanian, A., Torruella-Miller, I., Vassiliev, H., Voldy, M., Coldy, M., Wagner, A., Wang, B., Wheeler, J., Wu, Y., Ye, W.J., Zhao, J. and Jody, M., Mang, B., Wheeler, J., Wu, Y., Ye, W.J., Zhao, J. and Jody, M., Mang, B., Wheeler, J., Wu, Y., Ye, W.J., Zhao, J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (23-JUL-1998) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Jul 23, 1998 this sequence version replaced gi:3335015. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Only the first 118.8 kilobases of this clone are being submitted.
The remainder overlaps accession number AC005274 (WICGR project
L350).
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complement(932. ,1000)
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Homo sapiens putative prostate cancer susceptibility protein HPC2/ELAC2 gene, exon 17 and partial cds.
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Submitted (12-SEP-2000) Myriad Genetics, Inc., 320 Wakara Way, Salt
Lake City, UT 84108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 740)

Tavtigian, S. V., Simard, J. Teng, D.H.F., Baumgard, M., Beck, A., Camp, N.J., Carillo, A.R., Chen, Y., Dayananth, P., Desrochers, M., Dumont, M., Farnham, J.M., Frank, D., Frye, C., Ghafari, S., Gupte, J.S., Hu, R., Illev, D., Janecki, T., Kort, E.N., Lablanc, G., McArthur-Morrison, J., Pederson, A., Penn, B., Peterson, K.T., Reid, J.E., Richards, S., Schroeder, M., Smith, R., Snyder, S.C., Swedlund, B., Swensen, J., Thomas, A., Tranchant, M., and Cannon-Albright, L.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tavtigian, S.V., Simard, J., Teng, D.H.F., Baumgard, M., Beck, A., Tavtigian, S.V., Simard, J., Teng, D.H.F., Baumgard, M., Beck, A., Davtigian, S.V., Carillo, A.R., Chen, Y., Bayananth, P., Desrochers, M., Dumont, M., Farnk, D., Frye, C., Ghaffari, S., Gupte, J.S., Hu, R., Ilev, D., Janeck, T., Kort, E.N., Laity, K.E., Leavitt, A., Leblanc, G., McArthur-Morrison, J., Pederson, A., Penn, B. Peterson, K.T., Reid, J.E., Richards, S., Schroeder, M., Smith, R., Snyder, S.C., Swedlund, B., Swensen, J., Thomas, A., Tranchant, M., Woodland, A.-M., Labrie, F., Skolnick, M.H., Neuhausen, S., Rommens, J. and Cannon-Albright, L.A.
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                                                                                                                                     99932 TGTGTCCCACCTGCACGCAGATCACCACACGGTGAGTGTTGGGCTGGACCACACAAGCTGG
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                                                                                                           TGTGTCCCACCTGCACGCAGATCACCACACGGTGAGTGTTGGGCTGGACCACAAAGCTGG
                                                                                                                                                                                            541 AGCCTGGAGGAGGCACTGCCACGTTGAGTTGGCCTTTTGGCTGCGTCTTTTCCTCGCTT
                                                                                                                                                                                                                                                                              CCAAACTTGCCCAGAGCTTTTGTTACTCATCTCTGGCTAGGAAATGGTTTTTTGCAAAAC
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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99.9%; Pred. No. 1.3e-196;
Live 1; Mismatches 0; Indels 0; G
                                                                                                                                                                                                                                                                                                                  note="Single-stranded coverage.
                                                                                                                                                                                                                                                                                                                                 complement (25994. .2609)
/rpt family="purine-rich"
complement (26122. .26291)
/rpt family="MLTID"
26312. .26337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /rpt_family="(GGGAA)n"
complement(26576..26781)
/rpt_family="MER6B"
complement(26912..26990)
/rpt_family="MER21B"
26991..27290
                                                                                                                                                                                                                                                rpt_family="MLT1D"
:5816. .25895
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family="AluSx"
ement (211)
                                      /rpt_family="L1M4"
21799. .22104
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. .26480
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complement(27291. ...
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/rpt_family="LTR28"
28920. .29005
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                                                                                                         rpt_family="AluJo"
2151. .22562
                                                                                                                                                                                        'rpt_family="AluSq'
:485<u>2</u>. .25199
                                                                                                                                                 rpt_family="MSTA" 3978. .24287
                                                                                                                                                                                                                2485<u>2</u>. .25199
/rpt_family="L2"
complement(25697.
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29140. .29233
        complement (21101
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Tashiro, H., Yamazaki, M., Watanabe, K., Kumagai, A., Itakura, S., Fujimori, Y., Komiyama, M., Sugiyama, T., Irie, R., Otsuki, T., Sato, H., Wakamatsu, S., Ishii, S., Yamamoto, J., Isono, Y., Kawai. Hio, Y., Satto, K., Nishikawa, T., Kimura, K., Yamashita, H., Matsuo, K., Nakamura, Y., Sekine, M., Kikuchi, H., Kanda, K., Wagatsuma, M., Wurakawa, R., Kamehori, K., Takahashi-Fujii, A., Oshima, A., Sugiyama, A., Kawakami, B., Suzuki, Y., Sugano, S., Nagahari, K., Masuho, Y., Nagai, K., and Isogai, T., Sugano, S., NEDO human cDNA sequencing project Unpublished Unpublished Unbulsished Unbulsished Unbulsished Unbulsished Unbulsished Unbulsished Unbulsished Unbulsished Unbulsished Unbulsished Unbulsished Unbulsished Unbulsished Unbulsished Unbulsished Unbulsished Unbulsished Unbulsished Unbulsished Unbulsished Unbulsished Unbulsished Unbulsished Unbulsished Unbulsished Unbulsished Unbulsished Unbulsished Unbulsished Unbulsished Unbulsished Unbulsished Unbulsished Unbulsished Unbulsished Unbulsished Unbulsished Unbulsished Unbulsished Unbulsished Unbulsished Unbulsished Unbulsished Unbulsished Unbulsished Unbulsished Unbulsished Unbulsished Unbulsished Unbulsished Unbulsished Unbulsished Unbulsished Unbulsished Unbulsished Unbulsished Unbulsished Unbulsished Unbulsished Unbulsished Unbulsished Unbulsished Unbulsished Unbulsished Unbulsished Unbulsished Unbulsished Unbulsished Unbulsished Unbulsished Unbulsished Unbulsished Unbulsished Unbulsished Unbulsished Unbulsished Unbulsished Unbulsished Unbulsished Unbulsished Unbulsished Unbulsished Unbulsished Unbulsished Unbulsished Unbulsished Unbulsished Unbulsished Unbulsished Unbulsished Unbulsished Unbulsished Unbulsished Unbulsished Unbulsished Unbulsished Unbulsished Unbulsished Unbulsished Unbulsished Unbulsished Unbulsished Unbulsished Unbulsished Unbulsished Unbulsished Unbulsished Unbulsished Unbulsished Unbulsished Unbulsished Unbulsished Unbulsished Unbulsished Unbulsished Unbulsished Unbulsished Unbulsished Unbulsished Unbulsished Unbulsished Unbulsished Unbulsi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (Razusa-Kamatari, Kisarazu, Chiba 292-0812, Japan (Razusa-Kamatari, Kisarazu, Chiba 292-0812, Japan (B-mall:genomics@hri.co.jp, Tel:81-438-52-9975, Fax:81-438-52-3986) NBDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; CDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction: Hell:Research Institute (HRI) (supported by Japan (Rey Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: HRI and RAB; annotation: HRI and RAB.
                                                                          Homo sapiens CDNA FLJ36693 fis, clone UTERU2008901, highly similar to Homo sapiens putative prostate cancer susceptibility protein HPC2/ELAC2 mRNA.
                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                              insert sequence).
to mRNA, clone_lib:UTERU2
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/db_xref="taxon:9606"
/clone="WTERU2008901"
/tissue_type="uterus"
/clone_Tib="UTERU2"
/note="cloning_vector:_pME18SFL3"
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/product="putative prostate cancer susceptibility protein
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1; Mismatches 0;
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chromosome="17"
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Direct Submission

Submitted (14-FBB-2002) Sumio Sugano, Institute of Medical Science,
University of Tokyo, Laboratory of Genome Structure, Human Genome

(E-ners, Shirokame-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan

(E-mail:cdnal@ins.u-tokyo.ac.jp, Tel:81-3-5449-5286,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan, cDNA full insert sequencing: Research Association for Biotechnology: cDNA library construction, 5' - & 3'-end one pass sequencing: Departent of Virology and Human Genome Center, Institute of Medical Science, University of Tokyo (partly supported by Science and Technology Agency).
                                                                                                                                                                                                                                                                                                                                                                                                                                  oligo capping; fis (full insert sequence). Home sapiens hepatoma cell_line:HepG2 cDNA to mRNA, clone_lib:HEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryoča, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kawabata, A., Hikiji, T., Kobatake, N., Inagaki, H., Ikema, Y., Kokanco, S., Okiteni, R., Ota, T., Suzuki, Y., Obayashi, M., Nishi, T., Shibahara, T., Tanaka, T., Tanaka, T., Isogai, T. and Sugano, S. NEDO, human cDNA sequencing project
                                                                                              1164
                                                                                                                                                                   1165 Trecrerreagnicative riseració de academica de risera de conservado 1224
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                                                         697
                                                                                                                                   757
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1045 IGGCTGCGCTTTTTCCTCCGCTTCCAAACTTGCCCAGAGCTTTTGTTACTCATCTCTGGC
                                                                                        1105 TAGGAAATGGTTTTTTGCAAAACTCAACATAGTCCTTCTGCGCCACAAGAATGTCTTCTC
                                                                                                                                 TGTGGTGAGGCCACRTTTGGGCAGCTGTGCCGTCATTACGGAGACCAGGTGGACAGGGTC
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                                                                                                                                                                                                                             1225 TCTTGAATCTCACACGCCTGCTCAGCGGAAGCTTTGACCGGAT 1268
                                                                                                                                                                                                          TCTTGAATCTCACACGCCTGCTCAGCGGAAGCTTTGACCGGAT 801
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438 t
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Pred. No. 6.3e-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
db xref="taxon:9606"
/clone="HEP03495"
/cell_line="Hep62"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             vector:
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/clone_lib="HEP"
/note="cloning vector
                                                                                                                                                                                                                                                                                                                                                                                             AK074244.1 GI:18676795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 89.1%;
Matches 156; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (bases 1 to 2163)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     clone:HEP03495.
Homo sapiens
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Direct Submiston.

Direct Submiston.

Direct Submiston

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Submitted (04-JUL-2002) Takao Isogai, FLJ Project (HRI Team); 2-6-7

Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan

Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan

(E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)

NEDO human cDNA sequencing project supported by Ministry of

Economy, Trade and Industry of Japan; cDNA full insert sequencing:

Research Association for Biotechnology (RAB); cDNA library

construction: Helix Research Institute (HRI) (supported by Japan

Key Technology Center tec.); 5-6, 43-end one pass sequencing: RAB,

HRI, and Biotechnology Center, National Institute of Technology and

Evaluation; clone selection for full insert sequencing: HRI and

RAB; annotation: HRI and RAB.
                                                                                                                                                                                                           AK094333 2734 bp mRNA linear PRI 15-JUL-2002 Homo sapiens cDNA FLJ37014 fis, clone BRACE2010203, highly similar to Homo sapiens prostate cancer susceptibility protein HPC2/ELAC2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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Sugiyama,T., Irie,R., Otsuki,T., Sato,H., Wakamatsu,A., Ishii,S.,
Yamamoto,J., Isono,Y., Kawai-Hio,Y., Saito,K., Nishikawa,T.,
Kimura,K., Yamachita,H., Matsuo,K., Nakamura,Y., Sekine,M.,
Kikuchi,H., Kanda,K., Wagatsuma,M., Murakawa,K., Kanehori,K.,
Takahashi-Eujii,A., Oshima,A., Sugiyama,A., Kawakami,B., Suzuki,Y.,
Sugano,S., Nagahari,K., Masuho,Y., Nagai,K. and Isogai,T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Euteleostomi;
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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oligo capping; fis (full insert sequence).
Homo sapiens cerebellum cDNA to mRNA, clone_lib:BRACE2
845 CTGGGCACCTGGCTGTGTTTTGTGTCCCACCTGCAGAGATCACCACGG
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Pred. No. 6.4e-27;
1; Mismatches 18
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/clone lib="BRACE2"
/note="cloning vector: pMi
708 c 724 g 631
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/clone="BRACE2010203"
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ilarity 89.1%;
Conservative
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AF308694

SOURCE

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Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tavtigian, S.V., Simard, J., Teng, D.H.F., Baumgard, M., Beck, A., Cavtigian, S.V., Simard, J., Teng, D.H.F., Baumgard, M., Beck, A., Cavtillo, A.R., Chen, Y., Dayananth, P., Deerochers, M., Dumont, M., Farnham, J.M., Frank, D., Frye, C., Ghaffari, S., Gupte, J.S., Hu, R., Iliev, D., Janecki, T., Kort, E.N., Lairy, K.E., Leavitt, A., Leblanc, G., McArthur-Morrison, J., Pederson, A., Penn, B., Peterson, K.T., Raid, J.E., Richards, S., Schroeder, M., Smith, R., Snyder, S.C., Swellund, B., Swensen, J., Thomas, A., Tranchant, M., and Cannon-Albright, L.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /protein_id="AaG24916.1"
/db_xref="G1:10946489"
/translation="WMALCSLLRSAAGRTMSQGRTISQAPARRERPRKDPLRHLRTRE
KRGPSGGGGGPONTVXLLQVVAAGSRDSGAALYVFSEFNRYLFNCGEGVQRLMQEHKLKV
VRLDNIFLYRMHWSVVGGLSGNILTLKETGLRCVLSGPPQLEKYLBAIKIFSGPLKG
IELAVRPHSAPEYEDETMTVYQIPIHSEQRRGRHQPWQSPERPLSRLSPERSSDSESN
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APVLOKSTITHEGREILAEELGTPPDGAAFVVUSCPBESTIQPICKUNTPGRYGKAD
APVALVVHMAPESVLVUSRYQQMMERRGPDTQHLVLNENCASVHNLSGHKIQTCLNLI
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LQLPRPQSVOYOBRRRSVODPAPAERKSGYPEITFLGTGGSATBKIRNSATLVNISP
LOTSLLLDCGGGGTFGQLCRHYGDQVDRVLGTLAAVFVBHLHADHHTGLNILLQREQAL
ASLGKPLHPLLVVAPSQLKAMLQQYHNQCQBVLHHISMIPAKCLQEGAEISSPAVERL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (27-SEP-2000) Myriad Genetics, Inc., 320 Wakara Way, Salt Lake City, UT 84103, USA
               PRI 27-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note="similar to Homo sapiens HPC2/ELAC2"
AF308694 2893 bp mRNA linear
Gorilla gorilla ELAC2 (ELAC2) mRNA, complete cds.
AF308694

    2893
/organism="Gorilla gorilla"
/db_xref="taxon:9593"
    2893

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                                                                                AF308694.1 GI:10946488
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Bukaryota, Merazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Bukaryota; Merazoa; Chordata; Catarrhini; Hominidae; Homo.

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Tavtigian, S.V., Simard, J., Teng, D.H.F., Abtin, V., Baumgard, M., Beck, A., Camp, N.J., Carillo, A.R., Chen, Y., Dayananth, P., Desrochers, M., Dumont, M., Farnham, J.M., Frank, D., Frye, C., Ghaffari, S., Gupte, J.S., Hu, R., Iliev, D., Janecki, T., Kort, E.N., Latry, K.E., Leavitt, A., Leblanc, G., McArthur-Morrison, J., Pederson, M., Penn, B., Peterson, K.T., Reid, J.E., Richards, S., Schroeder, M., Smith, R., Snyder, S.C., Swedlund, B., Swensen, J., Tranchant, M., Woodland, A.M., Labrie, F., Skolnick, M.H., Neuhausen, S., Rommens, J. and Cannon-Albright, L.A.

A candidate prostate cancer susceptibility gene at chromosome 17p
ISSLIRTCDLEEFQTCLVRHCKHAFGCALVHTSGWKVVYSGDTMPCEALVRMGKDATL LITBATLEBOGGLEEBAVBKTHSTYSQAL SVGMRNNAEFTMLNHFSGRYAKVPLFSPNFN LKVGYAFDHMKVCFGOFFTMRKLI PFLKALFAGDIEBMEERREKRELRQVRAALLSGE LAGGLEDGEPQQKRAHTEEPQAKKVRAQ"
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Lake City, UT 84108, USA
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/product="putative prostate cancer susceptibility protein
HPC2/ELAC2"
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Pred. No. 6.4e-27;
1; Mismatches 18;
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/db_xref="taxon:9606"
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Matches 156; Conservative
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Rammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.

I (bases 1 to 2908)

Tavtigian, S.V., Simard, J., Teng, D.H.F., Abtin, V., Baumgard, M., Beck, A., Camp, N.J., Carillo, A.R., Chen, Y., Dayananth, P., Desrochers, M., Dumont, M., Farnham, J.M., Frank, D., Frye, C., Ghaffari, S., Gupte, J.S., Hulla, Y. Lilev, D.J., Janecki, T., Kort, E.N., Laity, K.E., Leavitt, A., Leblanc, G., McArthur-Morrison, J., Pederson, A., Penn, B., Peterson, K.T., Reid, J.E., Richards, S., Schroeder, M., Smith, K., Snyder, S.C., Swedlund, B., Swensen, J., Thomas, A., Tranchant, M., Moodland, A.M., Labrie, F., Skolnick, M.H., Neuhausen, S., Rommens, J. and Cannon-Albright, L.A.

A candidate prostate cancer susceptibility gene at chromosome 17p L. Nat. Genet. 27 (2), 172-180 (2001)
                                       / translation="WMALCSLLRSAAGRTWSQGRTISQAPARRERPRKDPLRHLRTRE
REPSGCSGGGRWTVYLQVVAAGSRDSGAALVVPSERNRYLFRGGGVQRLWGEHKLKV
ARLDNIFLIRMHWSNVGGLSGMILTLKETGLPKCVLSGPPQLEKYLEAIKIPSGPLK
ELAVREHSAPEXEDETWTVYQIPINEGRENGHQPMQSPRRELSBLSPERSBSESN
ENEPHLLPHGVSQRRGYRDSSLVVAFTCKLHKRGNFLVLKAKEMGLPVGTAAIAPITA
AVKDGKSITHEGRELILAELCTPPDPGAAFVVVECPDESFIQPICORNTFQRYGGKAD
APVALVVHMAPASVLVDSRYQQWMERFGPDTQHLVLNENCASHNLRSHKIQTGLNL
HPDIFPLLTGRRCKKEGPTLSVPWYQGECLLKYQLRPRRECASHNLRSHKIQTGLNL
LQLPPPQQSVQVEVRSAQDGPAPAEKKSQYPEII FLGTGSAFWKIRNVSATLVNISP
DTSLLLDCGECTFGQLCRYYGOVDRYLGTLAAVFVSHLHADHHTGLPSILLQFERAL
ASLGKRLHADHHTGLPSILLQFERALSSPAVERI
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LIHEATLEDGLEEEAVEKTHSTTSQAISVGMRMNAEFIMLNHFSQRYAKVPLFSPNFS
EKVGVAFDHMKVCFGDFPTMPKLIPPLKALFAGDIEEMEERREKRELRQVRAALLLSRE
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Pan troglodytes ELAC2 mRNA, complete cds.
AF308698
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Jacases 1 to 2908)

Tavtigian, S.V., Simard, J., Teng, D.H.F., Baumgard, M., Dayananth, P., Desrochers, M., Dumont, M., Farnham, J.M., Frank, D., Frye, C., Ghaffari, S., Gupte, J.S., Hu.R., Iliev, D., Janecki, T., Kort, E.N., Laity, K., Leavitt, A., Leblanc, G., McArthur-Morrison, J., Pederson, A., Penn, B., Peterson, K.T., Reid, J.E., Richards, S., Schroeder, M., Smith, R., Snyder, S.C., Swedlund, B., Swensen, J., Schroeder, M., Smith, R., Woodland, A.-M., Labrie, F., Skolnick, M.H., Neuhausen, S., Rommens, J. and Cannon-Albright, L.A.
Direct Submission

Direct Submission

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KRGPGGCSGGPNTVYLQVVAAGSRDSGAALYVFSEFNRYLFNCGEGIQRLMQEHKLKV ARLDNIFITRAHWSNVGGLSGMILTLKETGLPRCVLSGPPQLEKYLESAIKIFSGPLKG ELAVRPHSAPEYEDETWITVQIPIHESQRRGKHQPWQSPERPLSRLSPERSSDSSN ENBPHLEHGVSQRRGVRDSSLYVAFICKLHLKRGRIFLVLKAKEMGLEVGTAALAPIIA AVKDGKSITHBGREILAEELCTPPDDGAAFVVVECPDESFIQPICENATFQRYQGKAD
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LQLPNFQQSVQEYRRSAQDGPAPAEKRSQYPEIIFLGTGSAIPMKIRNVSATLVNISP
DTSLLLDCGEGTFGQLCRHYGDQVDRVLGTLAAVFVSHLHADHHTGLLNILLQRERAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /protein_id="AAG24920.1"
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ISSLLRTCDLEEFQTCLVRHCKHAFGCALVHTSGWKVVYSGDTMPCEALVRMGKDATL
LIHEATLEDGLEEEAVEKTHSTTSQAISVGMRMNAEFIMLNHFSQRYAKVPLFSPNFN
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 2908;
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Homo sapiens cDNA FLJ10530 fis, clone NT2RP2000985.
AK001392
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Pred. No. 6.4e-27;
1; Mismatches 18
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    2908
    /organism="Pan troglodytes"
/db_xref="taxon:9598"
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Best Local Similarity 89.1%;
Matches 156; Conservative 1
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               ACCESSION
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                                                                                                                               S Isogai, T. and Otsuki, T.

Isogai, T. and Otsuki, T.

Direct Submission

Submitted (16-FEB-2000) Takao Isogai, Helix Research Institute,
Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
(E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)

NEDO human CDNA sequencing project supported by Ministry of
International Trade and Industry of Japan; CDNA full insert
sequencing: Research Association for Biotechnology; CDNA library
construction, S - & 3'-end one pass sequencing and clone selection:
Helix Research Institute (supported by Japan Key Technology Center
etc.) and Department of Virology, Institute of Medical Science,
University of Tokyo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    / CUCULIA SCALCE - ""
/ CLEAR SCALE SARAGERTMSQGRTISQAPARRER PRKDPLRHIRTRE / CLEAR SLAGIO - ""
/ AL XTREE - ""WALLCELLERAAGRTMSQGRTISQAPARRER PRKDPLRHIRTRE / LTABLAL STORE - ""WALLCELLERAAGRTMSQGRTISQAPARRER PRKDPLRHIRTRE / RCGPSGCSGGPNTYVIQVVARGSRDSGAALYVPSEFRRYLFNGGEGVQRLMQEHKKV ARLDNIFLTRMHWSNVGGLSGMILTILKETGLPKCVLSGPPQLEKYLEAIKIFSGPLKG IELAMRPHASAPEYEDETMTVYQIPIHSEQRRGKHQPWQSPERCSSDSESN ENDPHLPHGVSGRRCVPDSSLVVAFICKLHLKRGNFLVLKAKEMGLPVGTAALPSITA AVKDGKSITHSGREILAELCTPPDPGAAFVVVECPDESFIQPICENATFORYQCKAD APVALVVHMAPASVLVDSRYQOMMERFGPDTQHLVLNNENCASVHNLRSHKIQTGLNLI HPDIFPLIVYMAPASVLVDSRYQOMMERFGPDTQHLVLNNENCASVHNLRSHKIQTGLNLI HPDIFPPLIVYARAQOVGRCLLKYQLRPRRRWQRDAITATGNPSEFIVBL QLPNFQQSVQEYRRSQDGPAPAEKRSQYPEIIFGTGGSAIPMKIRNVSATLVNISPD TSLLLDGGGGTFGQLCRHYGDOVDRVLGTLAAVFVSHLHADHHTGLPSILLQREBALA SLCKPLHPLLIVVARNQLKAMLQQYXNQCQEVLHHISM PAKCLQGGAEISSPANERLI
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KVGVAFDHMKVCLGDFPTMPKLIPPLKALFAGDIEEMEERREKRELRQVRAALLSREL
AGGLEDGSLSRSGPTQRSHRPRRSEPSEDLGDPELRRLCVFCPTHAPVSALLAGRS"
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Ono,Y., Takiguchi,S., Watanabe,S., Kimura,K., Murakami,K.,
Ishii,S., Kawai,Y., Saito,K., Yamamoto,J., Wakamarsu,A.
Nakamura,Y., Nagahari,K., Masuho,Y., Ninomiya,K. and Iwayanagi,T.
NEDO human cDNA sequencing project
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/organism="Homo sapiens"
/db_xer=taxon:9606"
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/clone="NT2R-2000995"
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/coll_line="NT2"
/coll_line="NT2"
/coll_line="NT2"
/coll_line="NT2"
/coll_soctor: pME18SFL3.mRNA from MT2 neprecursor cells after 2-weeks retinoic acid (RA)
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Pred. No. 6.4e-27;
1; Mismatches 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
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Best Local Similarity 89.1%;
Matches 156; Conservative 1
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/ codon start=1
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/ brotein id="cab34932.1"
/ db_xref="dg:21439090"
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                                                                                                                                                                                                                                                                                                                                                                     Tang, Y.T., Liu, C., Zhou, P., Asundi, V., Zhang, J., Zhao, Q.A., Ren, F., Xue, A.J., Yang, Y., Wehrman, T. and Drmanac, R.T.
Novel nucleic acids and polypeptides
Patent: WO 0222660-A 240 21-MAR-2002;
HYSEQ, INC. (US)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2997)
                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Submitted (29-JAN-2001) National Institutes of Health, Mammalian
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/db_xref="taxon:9606"
75._.2555
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1666 CTGGGCACCCTGGCTGCTGTTTGTGTCCCACCTGCACGCAGATCACCACACGG 1720

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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAL Plate: 2 Row: c Column: 13
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 7022621.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /trānslation="MWALCSLLRSAAGRTMSQGRTISQAPARRERPRKDPLRHLRTRE
KRGPSGCSGGPNTVYLQVVAAGSRDSGAALYVFSEFNRYLFNCGEGVQRLMQEHKLKV
ARLDNIFLTRNHWSNVGGLSGMILTLKETGLPKCVLSGPPGJEKYLEALKIFSGPLKG
IELAVRPHSAPEYEDETMYTVQIPITHSGQRRGKHQPWGSPERPLSPERSSDSELN
ENEPHILPHGVSQRRGYRDSSILVVAFTCKLHHLRGNFUYLKAKEMGLPVGTAAIAPIIA
AVKDGKSITHEGREILAEELCTPPPDPGAAFVVVECPDESFIQPICENATFQRYQGKAD
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/protein_id="AAH04158.1"
/db_xref="GI:13278771"
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DTSLLLDCGEGTFGQLCRHYGDQVDRVLGTLAAVFVSHLHADHHTGLPSILLQRERAL
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ISSLLRTCDLEEFQTCLVRHCKHAFGCALVHTSGWKVVYSGDTWPCEALVRMGKDATL
LIHEATLEDGLEEEAVEKTHSTTSQAISVGMRMNAEPIMLNHFSQRYAKVPLFSPNFS
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HPDIFPLLTSFRCKKEGPTLSVPMVQGECLLKYQLRPRREWQRDAIITCNPEEFIVEA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      contact: amadan@systemsbiology.org
Anup Madan, Rachel Dickhoff, Jessica Fahey, Stephanie Ford, Julia
Greene, Mark Ketteman and Anuradha Madan
                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
Submitted (01-MAR-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                            BC004158 3006 bp mRNA linear PRI 12-JUL
Homo sapiens, putative prostate cancer susceptibility protein,
clone MGC:2441 IMAGE:2820640, mRNA, complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Institute for Systems Biology
http://www.systemsbiology.org
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'clone lib="NIH MGC 7"
'lab_host="DH10B-R"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
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/organism="Homo sapiens"
/db_xref="LocusID:60528"
/db_xref="taxon:9606"
/clone="MGC:2441 IMAGE:2820640"
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1 (bases 1 to 3006)
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KEYWORDS
SOURCE
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ORIGIN
                                                                                                                                                                                          DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE
AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                          ACCESSION
                                                                                                    RESULT 12
                                                                                                                              BC004158
LOCUS
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COMMENT
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DTSLLLDCGEGTFGQLCRHYGDQVDRVLGTLAAVFVSHLHADHHTGLPSILLQRERAL
ASLGKPLHPLLVVAPNOLKAWLQQYHQCQEVLHHISMIPARCKLQEGARISSPAVBRL
ISSLLRTCDLEBEPQTCLVRHCKHAFGALVHTSGWKVYSGDTMPCGALVRMGKDATL
LIHBATLEDGLEBEPATEKTHSTTSQAISVGRRNNABEFIMLNHFSQRYAKVPLESBNFS
EKVGVAFDHMKVCFGDFPTMPKLIPPLKALFAGDIEBMERREKRELRQVRAALLSRE
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product=="putative prostate cancer susceptibility protein"
protein_id="AAH01939.1"
/db_xref="GI:L2804973"
                                                                                                                                                                                                                                                                                                                                             info@bogsc.bc.ca
Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield,
Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield,
Sueamna Chan, Readman Chiu, Chris Fylell, Brin Garland, Ran Guin,
Letticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo
Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven
Ness, Pawan Pandoh, Anna-Lilisa Prabhu, Parvaneh Saeedi, Jacqueline
Schein, Duane Smailus, Michael Smith, Lorraine Spence, Jeff Stott,
Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy,
George Yang, Scott Zuyderduyn, Marco Marra.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Clone distribution: MGC clone distribution information can be fount through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAL Plate: 9 Row: i Column: 17 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 7022621. Location/Qualifiers
Jene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1546 ATTCGAAATGTCAGTGCCACACTTGTCAACATAAGCCCCGACACGTCTCTGCTACTGGAC 1605
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                                                                                                                                                                                                                        cDNA Library Preparation: Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Genome Sequence Centre, BC Cancer Agency, Vancouver, BC, Canada
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /tissue type="Lung, small cell carcinoma"
/clone lib="NIH MGC 7"
/lab_host="DH10B-R"
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                                                                                             NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs.r@mail.nih.gov
Tissue Procurement: DCTp/DTP
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/db_xref="LocusID:66528"
/db_xref="taxon:9606"
/clone="MGC:4102 IMAGE:2820640"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 145.8; DB 9
Pred. No. 6.4e-27;
1; Mismatches 18
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806 c 853 q 598 t
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Best Local Similarity 89.19
Matches 156; Conservative
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AUTHORS
TITLE
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Direct Submission

Direct Submission

Lorect Submission

Submitted (04-JUL-2022) Takao Isogai, FLJ Project (HRI Team); 2-6-7

Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan

Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan

Kerusi-Ispenomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)

NEDO human cDNA sequencing project supported by Ministry of

Economy, Trade and Industry of Japan, CDNA full insert sequencing:

Research Association for Biotechnology (RAB); cDNA library

construction: Helix Research Institute (HRI) (supported by Japan

Key Technology Center etc.); 5- & 3'-end one pass sequencing: RAB,

HRI, and Biotechnology Center, National Institute of Technology and

Evaluation; clone selection for full insert sequencing: HRI and

RAB; annotation: HRI and RAB.

[Location/Qualifiers]
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Homo sapiens cDNA FLJ37368 fis, clone BRAMY2024530, highly similar to Homo sapiens prostate cancer susceptibility protein HPC2/ELAC2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             oligo capping; fis (full insert sequence).
Homo sapiens amygdala cDNA to mRNA, clone_lib:BRAMY2
clone:BRAMY2024530.
                                             Indels
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    89.1%; Pred. No. 6.4e-27; ive 1; Mismatches 18;
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Best Local Similarity 88.6%; Pred. No. 1.7e-26;
Matches 155; Conservative 1; Mismatches 19
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clone lib="BRAMY2"
'note="cloning vector: p
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/clone="BRAMY2024530"
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                                                 Matches 156; Conservative
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Similarity
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Direct Submission
Submitted (19-JUL-2002) Human Genome Sequencing Center, Department Submitted and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
Contact: hgsc-help@bcm.tmc.edu
Center project name: GYER
Center project name: GYER
Center clone name: GYER
Center clone name: GYER
Sequencing vector: Plasmid:
Sequencing vector: plasmid:
Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 1109154 bases at least Q40
Consensus quality: 116608 bases at least Q30
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TTCTTTCTTTTTGATGCCCAGCATTGTGTTGATGCATATCCTTAAAGGCTTCAGG 126993 GTTCCATGGATACTTCTTTGCTATAAAGAGGATGACACATGTAAAATCACCTTTATGGTT 217 [### ### ##############################	C 126630 8157 34593 bp DNA linear ROD 04-APR-2001 musculus putative prostate cancer susceptibility protein 62) gene, complete cds, alternatively spliced. 8157 musculus.	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus. I (sites) I sank, D.C., Swedlund, B., Dumont, M., Tavtigian, S.V., Simard, J., Teng, D.H.F.; Baumgard, M., Beck, A., Camp, N.J., Carillo, A.R., Chen, Y., Dayananth, P., Desrochers, M., Farnham, J.M., Frye, C., Ghaffari, S., Gupte, J.S., Hu, R., Iliev, D., Janeck, T., Kort, E.N., Eatty, K.E., Leavitt, A., Leblanc, G., Marthur-Morrison, J., Pederson, A., Penn, B., Peterson, K.T., Reid, J.E., Richards, S.,	Schroeder, M., Smith, R., Snyder, S.C., Swensen, J., Thomas, A., Tranchant, M., Woodland, AM., Labrie, F., Skolnick, M.H., Neuhausen, S. Rommens, J. and Cannon-Albright, L.A. Mouse Elac2-containing genomic DNA Unpublished Unpublished Unpublished Leak, D.C., Swedlund, B., Dumont, M., Tavtigian, S.V., Simard, J., Frank, D.C., Swedlund, B., Dumont, M., Farnham, J.M., Frye, C., Teng, D.H.F., Baumgard, M., Beck, A., Camp, N.J., Carillo, A.R., Ghaffari, S., Gupte, J.S., Hu, R., Iliev, D., Janacki, T., Kort, E.N., Laity, K.E., Leavitt, A., Leblanc, G., McArthur-Morrison, J., Latty, K.E., Leavitt, A., Leblanc, G., McArthur-Morrison, J., Schroeder, M., Smith, R., Snyder, S.C., Swensen, J., Thomas, A., Tranchant, M., Woodland, AM., Labrie, F., Skolnick, M.H.,	Neuhausen, S., Rommens, J. and Cannon-Albright, L.A. Direct Submission Submitted (109-FEB-2001) Myriad Genetics, Inc., 320 Wakara Way, Salt Lake City, UT 84108, USA Location/Qualifiers 134593
Db 127052 TTCTTTCTTCTGTCTTTGATGCCC Qy 158 GTTCCATGGATACTTCTTTGCTA'	218 126932 278 278 126876	Oy 338 AGGGGAGTGGCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTC		•	Tranchant, M., Smith, R. Tranchant, M., Woodlan Neuhausen, S., Rommens JOURNAL Unpublished AUTHORS Frank, D.C., Swedlund, Teng, D. H.F., Baumgard Chen, Y., Dayananth, P. Ghaffari, S., Gupte, J. Laity, K.E., Leavitt, A. Pederson, A., Penn, B., Schroeder, M., Smith, R. Tranchant, M., Woodlan	Neuhausen,S., Rommens TITLE Direct Submission JOURNAL Submitted (09-FEB-20) Lake City, UT 84108, FEATURES Location/Qua

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No. is the number of results predicted by chance to have a Pred.

AC005277 118788 bp DNA linear PRI 23-JUL-1998 Homo gapiens chromosome 17, clone hRPK.597_M_12, complete sequence.

AC005277.1 GI:3337311

RESULT 1 AC005277 LOCUS DEFINITION

Homo sapiens.

KEYWORDS SOURCE ORGANISM

ACCESSION VERSION

REFERENCE AUTHORS TITLE JOURNAL

ALIGNMENTS

Ношо

AC018999 | AC022819 | AC018738 | AC074185 |

AL645722 | AL354953 |

HSA524G17

AC018999 AC022819 Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 118788)
Birren, B., Fasman, K., Linton, L., Nusbaum, C. and Lander, E.
Homo sapiens chromosome 17, clone hRPK.597_M_12
Unpublished

AC023591 Homo sapi AC017038 Homo sapi AC060764 Homo sapi Continuation (3 of Homo sapi Homo sapi Papio cyn Human DNA Homo sapi Homo sapi Human chr Human chr Human DNA Human chr Human DNA Human DNA sapi sapi sapi sapi sapi Homo sapi Homo sapi Homo sapi Homo sapi Homo sapi sapi sapi sapi sapi sapi score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. Ното Homo Homo Ношо Homo Ношо Ношо Homo Homo Description AL355840 BAC010366 BAC022129 BAL589762 BAL121767 BAL1217 AC012386 | AL161871 | AC073228 1 AC090088 1 AP000753 1 AC090382 1 AL354720 1 AC092631 1 AC016000 1 AC069106 1 AC022539 1 AC021718 1 AC091772 | AC068015 | AC116934 | AL499582 | AC111187 | AC084264 | AC022448 | AC109993 | AC069541 AC0155 SUMMARIES AC060764 AC009771_2 AC012386_0 CNS01RHN AC068015 CNS01DSC DB 25.1 74089 25.1 208309 25.1 153185 25.1 178653 25.1 178980 25.1 184057 25.0 199882 24.9 191468 24.9 171779 Query Match Length 184338 65612 181532 59915 149679 24.8 24.8 24.8 24.8 0 124.6 124.4 124.2 124.2 124.2 124.2 124.2 123.4 123.2 123.2 123.2 123.2 123.2 123.2 Score 123.6 Result 80

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                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (10-JUL-1998) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
Research, 320 Charles Street, Cambridge, MA 02141, USA
Si (bases 1 to 118788)
Birren, B., Fasman, K., Linton, L., Nusbaum, C., Lander, E., Allen, N.,
Baker, J., Baldwin, J., Barna, N., Beckerly, R., Benn, J., Boathn, C.,
Boutwell, C., Brown, A., Gastle, A., Cenry, J., Cooke, P., Depayre, E.,
Devon, K., Dewar, K., Donelan, L., Etemadi, S., Ferreira, P.,
FitzHugh, W., Forrest, C., Funke, R., Gage, D., Gardyna, S.,
Gensheimer, S., Geraigery, K., Gilmartin, T., Grant, G., Hagos, B.,
Harris, K., Horton, L., Howland, J.C., Hui, L., Jacotot, L., Kann, L.,
Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K.,
Maldrim, J., Molla, M., Morris, W., Morrow, J., Mychaleckyj, J.,
Nachman, A., Nahf, R., Naylor, J., Niloff, M., O'Connor, T., Pavlin, B.,
Peterson, K., Riley, R., Roberts, D., Rossello, R., Shyam, R.,
Strickland, C., Subramanian, A., Torruella-Miller, I., Vassiliev, H.,
Cody, M., Wagner, A., Wang, B., Wheeler, J., Wu, Y., Ye, W.J., Zhao, J. and
                 Birren, B., Fasman, K., Linton, L., Nusbaum, C., Lander, E., Allen, N., Baker, J., Baldwin, J., Barna, N., Beckerly, R., Benn, J., Boatin, C., Bowor, K., Dewar, K., Castle, A., Cerny, J., Cooke, P., Depayre, E., Devon, K., Dewar, K., Donelan, L., Etemadi, S., Ferreira, P., Perrest, C., Furke, R., Gage, D., Gardyna, S., Gensheimer, S., Geraglery, K., Gilmartin, T., Garatt, G., Hagos, B., Harris, K., Horton, L., Howland, J.C., Hui, L., Jacotoc, L., Kann, L., Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., Meltrim, J., Molla, M., Morris, W., Morrow, J., Mychaleckyj, J., Nachman, A., Nahf, R., Naylor, J., Nioff, M., O'Connor, T., Paviln, B., Peterson, K., Riley, R., Roberts, D., Rossello, R., Roy, A., Stange-Thomann, N., Stilwell, J., Stojanovic, N., Stone, C., Strickland, C., Subramanian, A., Torruella-Miller, I., Vassiliev, H., Vo, A., Wagner, A., Wang, B., Wheeler, J., Wu, Y., Ye, W.J., Zhao, J. and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (23-JUL-1998) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Jul 23, 1998 this sequence version replaced gi:3335015.
All repeats were identified using RepeatMasker: Smit, A.F.A. &
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http://ftp.genome.washington.edu/RM/RepeatMasker.html
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clone=lib="RPCI-11 human BAC library"
195. -884
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/chromosome="17"
/map="17"
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2718. .347
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complement(4282. 4321)
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complement(4328. .4608)
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/rpt_family="MIR"
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237. .2713
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family="L2"
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/rpt_family="AluJb" complement(18530, .1856) /rpt_family

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family="L2"

rpt

complement (15838, .15893) /rpt family="MER91A"

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.15620)

complement (11928. .12108)

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.19065

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complement (19971.

family="LIME3A" ement(2000)

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AC026279 157159 bp DNA linear HTG 07-JUL-2000 Homo sapiens chromosome 15 clone RP11-321G12, WORKING DRAFT SEQUENCE, 12 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
Submitted (21-MAR-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 157159)
Waterston,R.H.
                                      * NOTE: This is a 'working draft' sequence. It currently consists of 12 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as truns of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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On Jul 7, 2000 this sequence version replaced gi:7523953
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chemistry: Dye-primer ET; 86% of reads Chemistry: Dye-primer ET; 86% of reads Chemistry: Dye-terminator Big Dye; 14% of reads Assembly program: Phrap; version 0.990319 Consensus quality: 148266 bases at least Q40 Consensus quality: 151490 bases at least Q20 Insert size: 165000; agarose-fp Insert size: 165000; agarose-fp Quality coverage: 4.15 in Q20 bases; sum-of-contigs Quality coverage: 3.96 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Center: Washington University Genome Sequencing Center
Center code: WUGSC
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unknown length
of 4742 bp in length
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bp in length
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unknown length
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of 5346 bp in length
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of 5622
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HTG; HTGS_PHASE1; HTGS_DRAFT.
Homo sapiens.
Homo sapiens
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                                                                                                           78133 AAGCTCTGAGGGACTGACGT 78152
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Waterston, R.H.
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                                                                                                                                                                                                                                                          note="Single-stranded coverage."
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28034. 280497
/rpt_family="LTR28"
                                                                                                                                                                                                                                                                  complement (25994. ...cov)
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complement (26122. .26291)
/rpt family="MLTID"
26312. .26337
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24852. .25199
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complement(25697. .25985)
/rpt_family="MITID"
25816. .25895
/rpt_family="AluSx"
complement(21348, .21e^^^\/rpt_family="AluSx"
                                rpt family="L1M4" (1799) .22700
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6456. .26480
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22151. .22562
/rpt_family="MSTA"
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28920. .29005
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29140. .29233
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Matches 500; Conservative
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Homo sapiens chromosome 15, clone RP11-321G12, complete sequence.
AC087525
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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                                                        Db 147933 GAGTAGCTGGGACTACAGATGCCCGCCACCACCAACTAAT 147975
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7345. .42412
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Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Changalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Gorde, S., Govdete, M., Graham, L., Grand-Pierre, N., Hagos, J., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kalse, K., Lakocque, K., Lamazares, R., Landers, T., Lehoccky, J., Levine, R., Lindblad-Toh, K., Liu, G., MacLean, C., Macdonald, P., Major, J., Matquis, N., Mathews, C., McCarthy, M., McEwan, P., McKernan, K., Meldrim, J., Meneus, L., Mihova, T., Menga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norban, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Plankhang, P., Piere, N., Schupback, R., Saman, S., Severy, P., Spencer, B., Stange-Thomann, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M., Young, G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (14-MAY-2002) Whitehead Institute/MIT Center for Genome Submitted (14-MAY-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street. Cambridge, MA 02141, USA On May 14, 2002 this sequence version replaced gi:20334597.

All repeats were identified using RepeatMasker:

Shit, A.F.A. & Green, P. (1996-1997)

http://f.p.genome.washington.edu/RM/RepeatMasker.html

Center: Whitehead Institute/ MIT Center for Genome Research
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------ Project Information
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complement (177. 301)
/rpt family="L3"
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/note="<30 qual SNGL region"
complement (599. .940)
/rpt_family="L3"
676. .681
/note="<30 qual SNGL region"
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'note≃"single clone coverage"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               302._.598
/rpt_family="AluJb"
495. .499
/note="<30 qual SNGL region"
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[156. .1179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note="<30 qual SNGL region"
195. .1228
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.275. .1283
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343. .1349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               organism="Homo sapiens"
db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Center clone name: 321_G_12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Center project name: L11919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     rpt_family="AT_rich"
238. .1245
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/rpt_family="(A)n"
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/note="<30 qual SNGL region"

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Db 116995 GAAAAAATATTTGAGACTCCCAAGACCAGCAGAGAGATTATTATACAGAATATAAGAA 116936
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26.2%; Score 131; DB 9; Length 157590; 63.3%; Pred. No. 4.2e-23; tive 0; Mismatches 125; Indels 1;
                                                                                                                                                                                                                                                  complement (3653. .3947)
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complement (3948. .4149)
/rpt family="Tigger3 (Golem)"
complement fare
                                                 2239. .2243
/note="<30 qual SNGL region"
2329. .2335
                               note="<30 qual SNGL region"
                                                                                                                                                                                                                    complement (3580. .3652)
'rpt_family="Tigger3(Golem)"
qual SNGL region'
                                                                                                    note="<30 qual SNGL region
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4372. .14400
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'rpt_family="Aluy"
                                                                                                                                  /rpt_family="AT_rich"
complement(2683_.2961)
/rpt_family="Aludo"
complement(2969,.3579)
/rpt_family="LiM4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0133. .10286
rpt family="L2"
complement (10284. .10408)
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complement(14985, .15197)
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598. .8741
                                                                                                                                                                                                                                                                                                                                                              .4279)
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4891. .14984
                                                                                                                                                                                                                                                                                                                                                                                                             rpt_family="AT_rich"
omplement(50707.518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               rpt_family="AT_rich"
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                                                                                                                                                                                                                                                                                                                                        rpt_family="LipAl3"
omplement(4211, .427
                                                                                                                                                                                                                                                                                                                                                                        family="LiPA15"
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1547_.9455
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family="MER46B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      rpt_family="AluJb"
456. .9578
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0905. .11082
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omplement(11814.
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4833. .14852
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0484. .10588
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                   .2220
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     note="<30
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Best Local Similarity 63.33
Matches 217; Conservative
                                                                                                                        repeat_region
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                                                         Db 116755 TCTCGGCTCACTGCAACCTCCGCCTCCTGGGTTAAAGTGATTCTCCTGCCTCAGCCTCCC 116696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 171418)
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                                                                                                                                                                                  Db 116815 TTTGTTTTGTTTTGAGACAGAGTCTCACTCTGTTGCCCAGGCTGGAGTGCAGTGGCACGA 116756
                                                                                                                                                                                                                                              253 TTTCGACTCACCGCAACCTCCGCCTCC-GCGCTTAAGCGATTCTCCTGCCTCAGCCTCCC 311
AC023591 171418 bp DNA linear H
Homo sapiens chromosome 15 clone RP11-768L13 map 15,
IN PROGRESS ***, 2 ordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                       Db 116695 GAGTAGCTGGGACTACAGATGCCCGCCACCACCACTAAT 116653
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Homo sapiens chromosome 15, clone RP11-768L13
Unpublished
                                                                                                                                                                                                                                                                                                                                                                    312 AAGTAGCTGGGACTACAAGCTCGGGACACCACGTAAAATGAT 354
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Zody, M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DEFINITION
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JOURNAL
REFERENCE
AUTHORS
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TITLE
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LOCUS
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KEYWORDS
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Roman, J., Roy, A., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M. Warn, D., Young, G., Zainoun, J., Direct Submission

L. Submitted (18-AUG-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Apr 20, 2002 this sequence version replaced gi:15291064.

All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)

http://ftp.genome.washington.edu/RM/RepeatMasker.html

Center: Whitehead Institute/ MIT Center for Genome Research
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  73 AAAGCTGAGGCTCTGAGAGGTCAAGATCACGCAGCTAACAAATGAGCCAAGACTCTTGCT 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13 GAATICTATATICTGAAGTAGGAGATACTGTTATIGCTGTTATIACATTTTACACATAAG 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NOTE: This is a 'working draft' sequence. It currently consists of 2 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor. This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.
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Pred. No. 4.2e-23;
0; Mismatches 125; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Web site: http://www-seg.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21023 21122: gap of 100 bp
21123 171418: contig of 150296 bp in length.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="RPCI-11 Human Male_BAC"
39250 c 39907 g 46239 t 100 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Center clone name: 768_L_13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Center project name: L6849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="taxon:9606'
/chromosome="15"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Center code: WIBR
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DEFINITION

RESULT 5 AC017038

ACCESSION

REFERENCE AUTHORS TITLE

JOURNAL REFERENCE AUTHORS TITLE JOURNAL

COMMENT

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Gaps
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0
si gap of unknown length
contig of 6723 bp in length
contig of 7719 bp in length
contig of 7719 bp in length
gap of unknown length
contig of 7699 bp in length
gap of unknown length
contig of 8859 bp in length
gap of unknown length
contig of 11813 bp in length
gap of unknown length
contig of 11813 bp in length
gap of unknown length
contig of 14814 bp in length
gap of unknown length
contig of 14814 bp in length
contig of 16327 bp in length
contig of unknown length
contig of unknown length
gap of unknown length
contig of 18349 bp in length
gap of unknown length
contig of 1837 bp in length
contig of 1837 bp in length
gap of unknown length
gap of unknown length
gap of unknown length
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Pred. No. 1.7e-22;
0; Mismatches 99;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note="assembly_name:Contig19"
4492. .62210
note="assembly_name:Contig20"
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note="assembly_name:Contig12"
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note="assembly_name:Contig13"
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note="assembly_name:Contig16"
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note="assembly_name:Contig21"
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note="assembly_name:Contig10"
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21943. .141936
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142037. .180707
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/note="assembly_name:Contig24
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'note="assembly_name:Contig9"
                                                                                                                                                                                                                                                                                                                                                                                                                                ....2076
note="assembly_name:Contig8"
                                                                                                                                                                                                                                                                                                                                           1. .180707
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="8"
                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                             clone="RP11-313B2"
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105516. .121842
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65.5%;
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105515: 0
121842: 0
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Best Local Similarity 65.5
Matches 188; Conservative
 47569
47669
54392
544392
62211
70010
70110
78969
790882
90882
                                                                                                                                                                                                                                                                   121943
141937
142037
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ORIGIN
                                                                                                                                                                                                                                                                                                                        FEATURES
                  ACUL/U38
180707 bp DNA linear HTG 07-JUL-2000
Homo sapiens chromosome 8 clone RP11-313B2, WORKING DRAFT SEQUENCE,
20 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                           Louis,
                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo. 1 (bases 1 to 180707) Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                    Submitted (09-DEC-1999) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. MO 63108, USA
On Jun 16, 2000 this sequence version replaced gi:7230978.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NOTE: This is a working draft' sequence. It currently consists of 20 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequencing vector: plasmid; $
Chemistry: Dye-primer ET; $ of reads
Chemistry: Dye-traminator Big Dye; $ of reads
Chemistry: Dye-traminator Big Dye; $ of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 168786 bases at least Q40
Consensus quality: 17486 bases at least Q20
Consensus quality: 17496 bases at least Q20
Insert size: 200000; agarose-fp
Insert size: 200000; agarose-fp
Insert size: 348 in Q20 bases; agarose-fp
Quality coverage: 3.86 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                            Center: Washington University Genome Sequencing Center Center code: WUGSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2076: contig of 2076 bp in length 2176: gap of unknown length 4769: contig of 2593 bp in length 4869: gap of unknown length 7558: contig of 2689 bp in length 7658: gap of unknown length 10945: contig of 3287 bp in length 11495: gap of unknown length 13945: contig of 2900 bp in length 14945: gap of unknown length
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length
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                                                                                                                                                                                                                                             The sequence of Homo sapiens clone Unpublished
                                                                                                     AC017038.6 GI:8568131
HTG; HTGS PHASE1; HTGS_DRAFT.
HOMO sapiens
HOMO sapiens
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O'Connor, T., O Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phukkhang, P., Pierre, N., Raymond, C., Retta, R., Rise, C., Rogov, P., Royan, J., Roy, A., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talamas, J. Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Zimler, A. wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         one lib="RPCI-11 Human Male BAC"
.87
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complement(167. .417)
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complement(566. .760)
/rpt_family="LiMC5"
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Center clone name: 626_A_5
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1947. .1951
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/db_xref="taxon:9606"
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1391. .1480
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complement(937...
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Submitted (20-APR-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

Research, 320 Charles Street, Cambridge, MA 02141, USA

Barran, B. Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barran, N., Bastien, V., Bloom, T., Boguslavkiy, L., Boukhqalter, B., Comerarata, J., Chang, J., Chazarach, E., Choepel, Y., Collymore, A., Cooke, P., Dehrellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Grad, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Horton, L., Hulme, W., Iliev, J., Johnson, R., Jones, C., Kamat, A., Karaasa, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, MacCarthy, M., Meldrim, J., Maneus, L., Mihova, T., Matthews, C., McCarthy, M., Meldrim, J., Maneus, E., Mihova, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C.H.,
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                        Db 174248 ATGTGACTATCAGTTAAACAATAAGAAAGTTATTTCACATTATTTGTAGTATGTCCAAAA 174307
                                                                                                                Db 174368 CAGAGTCTCGCTCTGTCACCCAGGCTGGAGTGCAATGGCATGATCTCAGCTCACTGCAAG 174427
                                                                                                                                                                                                                                                                 Db 174428 TTCCGCCTCCCGGGTTCTGCCATTCTCCTGCCTCAGCCTCCCAAGTAGCTGGGACTACAG 174487
                                                                                                                                                                                                                              270 CTCCGCCTCCGCGCTTAAGCGATTCTCCTGCCTCCAGCCTCCCAAGTAGCTGGGACTACAA 329
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Homo sapiens chromosome 8, clone RP11-626A5, complete sequence.
ACO60764
     90 AGGTCAAGATCACGCAGCTAACAAATGAGCCAAGACTCTTGCTTTAGAGCTTGTCCTCTA 149
                                                                                                                                                    210 CAGGGTCTCGAGGTGTCACCCAGGCTGGAGTGCAGTGGCGCGATTTCGACTCACCGCAAC
                                                                             330 GCTCGGGACACCACGTAAAATGATCAAGTTCTAACATGTATGCATA 376
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Homo sapiens chromosome 8, clone RP11-626A5
Unpublished
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Complement (2854.3158)
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complement (3899.3904)
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complement (3934.4089)
/rpt_family="FRAM"
complement (3934.3976)
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                                                                                                                                                                                                                    'note="Probably C, possibly A"
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1381. .14073
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omplement(11343, .11622)
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1623, .11768
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omplement (10745. .10865)
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complement(5802. .5971)
frpt_family="MIR"
complement(2310. .2617)
/rpt_family="Aluy"
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119. 972
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omplement(10091.
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3467. .13778
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3780. .13803
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1305. .11342
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1163. .11304
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Continuation (3 of 4) of AC009771 from base 200001 (AC009771 Homo sapiens chromosome 12
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Pred. No. 6.4e-22;
0; Mismatches 46; Indels 0;
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65.5%; Pred. No. 1.7e-22;
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/rpt_family="AluJo"
14374. .14663
/rpt_family="LIMB4"
14669. .15128
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ACO12386_1 10
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NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a "working draft' sequence. It currently consists of 24 contigs. The true order of the pieces is not known and their order in this sequence record is
               Sequencing vector: Plasmid; Chemistry: Dye: 100% of reads Sequencing vector: M13; Chemistry: Dye-terminator Big Dye: 100% of reads Assembly program: Phrap; version 0.990329 Consensus quality: 342731 bases at least Q40 Consensus quality: 34650 bases at least Q20 Estimated insert size: 170200; sum-of-contigs estimation Quality coverage: 6x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                    arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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/chromosome="12"
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I (bases it co 352204)

Murny, D. M., Adama, C., Adio-Oduola, B., Aliceman, F. Alien, C., Alabbrooks, S. L., Amaratunge, H. C., Are, J. R., Ayele, M., Benks, T., Barbarda, J., Bencon, J., Bimage, K., Blankenburg, K., Bonnin, D., Barbarda, J., Bencon, J., Bimage, H. C., Are, J. Rowis, B. Bryant, N. P., Bunch, D., Burkett, C., Burrell, K. L., Byrd, N. C., Carron, T. F., Carrer, M., Cavazos, S. R., Chacko, J. Chavez, D., Chen, G., Chen, R., Chen, R., Chen, R., Chen, R., Chen, R., Chen, R., Chen, R., Chen, R., Chen, C., Coyle, M. D., Dathorne, S. R., David, R., David, R., Delaney, K. R., Delagar, D., Edwards, C. C., Durbh, H. H., Delaney, R. R., David, R. J., Delaney, R. R., David, R. J., Delaney, R. R., David, R. J., Delaney, R. R., David, R. J., Earnhart, C., Edgar, D., Edwards, C. C., Elbaj, C., Becotto, M., Falls, T., Ferraguto, D., Flagg, N., Ford, J. Garza, N., Hernandez, J. Hernandez, C., Harris, K. Harris, K. Harris, K. Harris, K. Harris, K. Harris, R. Hawes, A., Harnandez, J. Harris, R. House, M., Gluse, M., Holloway, C., Hollins, B., Henrandez, C., Harris, K. Hogues, M., Holloway, C., Hollins, B., Henrandez, C., Hodgson, A., Hogues, M., Holloway, C., Hollins, B., Lacks, B., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C., Krafson, B., Yilly, M., Lad, B., Lewis, L. C., Lewis, L., Li, J., Li, Z., Lichtarge, O., Liedt, C., Liu, J., Liu, W., Loulesged, H., Massey, E., Mawhinsy, E., Matchin, R., Martin, R., Massey, E., Mawhinsy, E., Matchin, R., Martin, R., Massey, E., Mawhinsy, E., Matchin, R., Martin, M., Mel, J., Moster, M., Nolyedo, R., Pace, A., Payton, B., Peerz, J., Rockerson, E., Peters, J., Li, J., Makeshwari, N., Nolsedo, R., Pace, A., Payton, B., Peerz, J., Peters, J., Taylor, C., Taylor, T., Telffod, B., Thomas, N., Tang, H., Suterer, S., Scott, G., Hanner, S., Warning, S., Warning, S., Warning, S., Warning, S., Warning, S., Warning, S., Warning, S., Warning, S., Warning, S., Warning, S., Warning, S., Warning, S., Warning, S., Warning,
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Submitted (27-0CT-1999) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
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                                                                                                                                             Eukaryoča, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Drafting Center Code: BCM
Contact: hgsc-help@bcm.tmc.edu
------- Project Information
Center project name: HMPZ
Center clone name: RP11-642P15
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SEQUENCE, 24 unordered pieces.
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Human chromosome 14 DNA sequence BAC R-66E7 of library RPCI-11 from chromosome 14 Of Homo sapiens (Human), complete sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
Heilig, R., 1961.1.J.L., Vico, V., Dasilva, C., Robert, C., Wincker, P., Brottier, P., Cattolico, L., Barbe, V., Pelletier, E., Artiguenave, F., Levy, M., Eckenberg, R., Brulls, T., deBerardinis, V., Cruaud, C., Sequencing of the human chromosome 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
Submitted (02-MAY-2001) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29761
                                                                                                                                                                                                                                                                        29762 GCAACCTCCGCCTCCAGGTTCAAGAGATTCTCCTGCCTCAGCCTCCCGAGTAGCTGGGAC 29821
                                                                                                                                                                                                                                                        324
                                                                                                                            TTGTTTTGTTTTGTTT 204
                                                                                                                                                                                       205 TGAGACAGGGTCTCGAGGTGTCACCCAGGCTGGAGTGCAGTGGCGCGATTTCGACTCACC 264
                                                                                                Gaps
                                                                                                                                                                                                          29702 TTAGACAGAACCTTGCCCTGTCACCCAGGCTGGAGTGCCACGATGGCACGATATTGACTCACT
                                                                                                                                                                                                                                                      265 GCAACCTCCGCCTTCCGCGCTTAAGCGATTCTCCTGCCTCAGCCTCCCAAGTAGCTGGGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                On May 7, 2001 this sequence version replaced gi:13509291.
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0
                                                                 Length 110000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Assembly program: Phrap; version 2.0
Quality coverage: 8.50x in Q20 bases; sum-of-contigs
                   4540 others
                                                                                             Indels
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                                                            Query Match 25.3%; Score 126.4; DB 2; Best Local Similarity 77.0%; Pred. No. 6.4e-22; Matches 154; Conservative 0; Mismatches 46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Web site: http://www.genoscope.cns.fr/
Contact: SeqRef@genoscope.cns.fr
/clone="RP11-642P15"
73601 c 73327 g 101345 t
                                                                                                                           CTCTATTCTTGCTTTTCTTTCCAAAAACACTACAATTT
                                                                                                                                                                                                                                                                                                                                                29822 TACAGGCAAGCGCCACCACG 29841
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AL161871
AL161871.6 GI:13990336
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Range : bases
                                                                                                                                                                                                                                                                                                                   TACAAGCTCGGGACACCACG 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (bases 1 to 148068)
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1435
6761
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                BASE COUNT
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CNS01RHN
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Human chromosome 14 DNA sequence BAC R-382E15 of library RPCI-11
from chromosome 14 of Homo sapiens (Human), complete sequence.
AL355840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens

Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Bukaryota, Metazoa, Chordata, Catarrhini, Hominidae, Homo.

(Dases 1 to 17993)
Heilig,R., Petit,J.L., Vico,V., Dasilva,C., Robert,C., Wincker,P.,
Brottier,P., Cattolico,L., Barbe,V., Pelletier,E., Artiguenave,F.,
Gyapay,G., Saurin,W. and Weissenbach,J.
Sequencing of the human chromosome 14
Unpublished
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BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     89216 TTTTGTTTTGTTTTGTTTTTTAGACAGAGTCTCGCTCTGTCACCCCAGGCTGGAGT 89275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             89335
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Downstream BAC (overlapping the SP6 end) : R-66E7 (AC=AL161871)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181 TITITGITITGITTTGTTTTGAGACAGGGTCTCGAGGTGTCACCCAGGCTGGAGT 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       89336 CCTCAGCCTCCCAAGTAGCTGGGACTACAGGCACGCCACCCATGCCCAACTGAT 89390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GCAGTGGCGCGATTTCGACTCACCGCAACCTCCGCCTCC-GCGCTTAAGCGATTCTCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          89276 GCAGTGGCGAGATCTCGGCTCACTGCAACCTCCAACTCCTGGGTTCAAGCGATTCTCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 126.2; DB 9; Length 148068;
Pred. No. 7e-22;
0; Mismatches 23; Indels 1;
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On Jun 7, 2000 this sequence version replaced gi:7799397.
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Quality coverage: 9.72x in Q20 bases; sum-of-contigs
                                                                                                                                                >= 40 : 98
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                                                                                                                                          Percentage of bases with a quality value
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Contact: SeqRef@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                           /clone lib="RPCI-11"
28188 c 25806 g 41094
                                                                                                                                                                                                                                  /organism="Homo sapiens"
                                                                                                                                                                                                                                                       /db_xref="taxon:9606"
/chromosome="14"
                                                                                                                                                                  Location/Qualifiers
1. .148068
                                                                                                                                                                                                                                                                                                                   /clone="R-66E7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AL355840.2 GI:8346754
HTG; HTGS_ACTIVEFIN.
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Best Local Similarity 86.3%;
Matches 151; Conservative
10635
14123
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72041
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4 (bases 1 to 115396)
DOE Joint Genome Institute and Stanford Human Genome Center.
                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="5"
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Center Code: JGI
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1. .115396
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SHGC-9796 G11325
                                                                                                                                                                                                                                                     WI-30358 G24410.
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Best Local Similarity
Matches 145; Conservat
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Homo sapiens chromosome 5 clone CTD-2044J15, complete sequence.
AC010366
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Direct Submission
Submitted (15-SEP-1999) Production Sequencing Facility, DOE Joint Segmen Institute. 2800 Mitchell Drive, Walnut Creek, CA 94598, USA (bases 1 to 115396)
DOE Joint Genome Institute and Stanford Human Genome Center.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 115396)

DOB Joint Genome Institute and Stanford Human Genome Center.

Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Db 172522 GCAGTGGCGAGATCTCGGCTCACTGCAACCTCCAACTCCTGGGTTCAAGCGATTCTCCTG 172463
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Submitted (09-JUN-2001) DOE Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94598, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TTGTTTTGAGACAGGGTCTCGAGGTGTCACCCAGGCTGGAGT 240
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Identified using the e-PCR software (G. Schuler)"
33215 c 36220 g 61553 t
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                                                                                                                                                                                                                                               le of bases with a quality value >= 40
Location/Qualifiers
1. .179937
                                                                                                                                                                                                                                                                                                                                                   /clone="R-382E15"
/clone lib="RPCI-11"
33688. .33899
/note="matching EMBL:N23600
                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="14"
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                 quality chart bases
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Matches 151;
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Homo sapiens chromosome 5 clone CTD-2183B18, WORKING DRAFT
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2 (bases 1 to 214139)

DOE Joint Genome Institute.

Direct Submitssion

Submitted (26-JAN-2000) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA

On Apr 20, 2001 this sequence version replaced gi:9954660.
Direct Submission
Submitted (21-701-2001) DOE Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94598, USA
On Jul 21, 2001 this sequence version replaced gi:14333753.
Draft Sequence Produced by DOE Joint Genome Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

    (bases 1 to 214139)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Db 31535 AGTACAGTGGCACGATCTCGGCTCACTGCAAGCTCCGCCTCCCAGGTTCAGCCATCTCCC 31476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      238 AGTGCAGTGGCGCGATTTCGACTCACCGCAACCTCCGCCTTCAGGCGATTCTCC 297
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     298 TGCCTCAGCCTCCCAAGTAGCTGGGACTACAAGCTCGGGACACCACGTAAAAATGAT 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    178 CAATTITIGITITIGITITIGITITIGAGACAGGGTCTCGAGGTGTCACCCAGGCTGG
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0
                                                                                                                                                                www.jgi.doe.gov
Finishing Completed at Stanford Human Genome Center
www-shgc.stanford.edu
woulity: Phrap Quality >=40 99.6% of Sequence;
Estimated Total Number of Errors is 0.4.
STS Content:
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HTGS HTGS PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
HOMO sapiens.
HOMO sapiens
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Center Project Name: 697863
Center clone name: CITB-H1_2183B18
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Submitted (19-FBB-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
hunquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Feb 11, 2002 this sequence version replaced gi:18649769.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ALS89762 74089 bp DNA linear PRI 09-FEB-2002
Human DNA sequence from clone RP11-396D18 on chromosome 1, complete
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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77: gap of unknown.
91: contig of 6314 bp in length.
91: gap of unknown length.
96: contig of 1975 bp in length.
66: gap of unknown length.
6222: contig of 8356 bp in length.
1522: gap of unknown length.
1528: gap of unknown length.
91807: contig of 6706 bp in length.
91807: contig of 3379 bp in length.
100081: contig of 1379 bp in length.
100081: contig of 12514 bp in length.
112695: gap of unknown length.
112695: gap of unknown length.
112789: gap of unknown length.
12489: gap of unknown length.
12489: contig of 11594 bp in length.
14381: contig of 26052 bp in length.
17394: contig of 26053 bp in length.
17394: contig of 26053 bp in length.
17394: contig of 26053 bp in length.
17394: contig of 42645 bp in length.
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/clone_lib="CalTech human BAC library D"
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Pred. No. 8.5e-22;
0; Mismatches 32
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/chromosome="5"
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Direct Submission
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               Consensus quality: 177232 bases at least 040
Consensus quality: 199777 bases at least 030
Consensus quality: 199769 bases at least 030
Consensus quality: 199769 bases at least 030
Estimated insert size: 121000; pulse field gel estimation
Estimated insert size: 210239; sum-of-contigs estimation
Quality coverage: 7.99 in 020 bases; pulse field gel estimation
Quality coverage: 4.6 in 020 bases; sum-of-contigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 40 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* truns of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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          This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (1.e., phred quality = 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at the feature from part of the feature from part of bacterial clone contigs of human chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping Group, Further information can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human chromosome 14 DNA sequence BAC C-2593121 of library CalTech-D from chromosome 14 of Homo sapiens (Human), complete sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                     RP11-396D18 It may be shorter because we sequence overlapping sections only once, except for a short overlap.
The true left end of clone RP11-175B9 is at 72090 in this sequence. The true right end of clone RP11-572A16 is at 2000 in this
                                                                                                                                                                                                                                                                                                                        http://www.sanger.ac.uk/HGP/Chui
RPI1-396D18 is from the library RPCI-11.2 constructed by the group
of Pieter de Jong. For further details see
http://www.chori.org/bacpac/home.htm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo. I (bases 1 to 208309)
Heliig, R., Petit, J.L., Vico, V., Dasilva, C., Robert, C., Wincker, P., Brottier, P., Cattolico, L., Barbe, V., Pelletier, E., Artiguenave, F.,
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only a small overlap as described above.
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/clone lib="RPCI-11.2"
14221 c 14800 g 24111 t
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/db_xref="taxon:9606"
/chromosome="1"
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Matches 155; Conservative
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CNS01DSC/c
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ORIGIN
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KEYWORDS
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BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
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Upstream BAC (overlapping the T7 end) : R-1074012 (AC=AL049828)
Downstream BAC (overlapping the SP6 end) : R-34018
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Levy, M., Eckenberg, R., Bruls, T., deBerardinis, V., Cruaud, C., Gyapay, G., Saurin, W. and Weissenbach, J.
Sequencing of the human chromosome 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   146 TCTATTCTTGCTTTTCCTTTCCAAAAACACTACAATTTTTGTTTTGTTTTGTTTTT
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Identified using the e-PCR software (G. Schuler)"
70845 a 38028 c 36323 g 63113 t
                                                                                                                                                                                                                                                                                   - Web : www.genoscope.cns.fr)
On May 7, 2001 this sequence version replaced gi:12580631.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Assembly program: Phrap; version 2.0
Quality coverage: 5.83x in Q20 bases; sum-of-contigs
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Center: Genoscope / Centre National de Seguencage
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Pred. No. 9.6e-22;
0; Mismatches 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Web site: http://www.genoscope.cns.fr/
Contact: SeqRef@genoscope.cns.fr
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/db_xref="taxon:9606"
/chromosome="14"
/clone="C-2593121"
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On Jul 27, 2000 this sequence version replaced gi:8440040.
                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo. 1 (bases 1 to 153185) Waterston, R.H.
                                                                                                                                       AC073228 153185 bp DNA linear HTG 02-, Homo sapiens chromosome 11 clone RP11-660B16, WORKING DRAFT SOCIENCE, 40 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NOTE: This is a 'working draft' sequence. It currently consists of 40 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequencing vector: plasmid; 0% Chemistry: Dye-primer ET; 100% of reads Chemistry: Dye-terminator Big Dye; 0% of reads Chemistry: Dye-terminator Big Dye; 0% of reads Assembly program: Phrap; version 0.990319
Consensus quality: 138961 bases at least Q40
Consensus quality: 138961 bases at least Q20
Consensus quality: 141663 bases at least Q20
Insert size: 191000; agarose-fp
Insert size: 1949285; sum-of-contigs
Quality coverage: 2.76 in Q20 bases; sum-of-contigs
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Center code: WUGSC
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1218: gap of unknown le

2910: gap of unknown le

3010: gap of unknown le

4398: contig of 1388 br

4398: contig of unknown le

5572: contig of unknown le

5672: gap of unknown le

7162: gap of unknown le

8864: contig of 13702 br

8864: contig of 13702 br

8864: contig of 1512 br

10576: gap of unknown le

10576: gap of unknown le

112553: gap of unknown le

12553: contig of 1377 br

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HTG; HTGS PHASE1; HTGS_DRAFT.
HOmo sapiens
Homo sapiens
Db 74122 TACAGGCACCTGCCACCATG 74103
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Db 152615 ACGAAGCTCTGTTTTGATGTGTTTTTTATGCCGTGACTTTGTATGCAACACACTCAACTC 152674

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Db 152735 GTAGTGGCGCATCTCGGCTCACCAGCTCTGCCTCCGGGTTCACGCCGTTCTCCTGC 152794
241 GCAGTGGCGCGATTTCGACTCACCGCAACCTCCGCCTCCGCGCTTAAGCGATTCTCCTGC 300
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2517 2517 2517 2517 2517 2517 2517 2518 2518 2518 2518 2518 2518 2518 2518	ALIGNME -09-564-805-3 Sequence 3, Application US/09564805 Patent No. 6333403 GAPERAL INFORMATION: APPLICANT: Tavtigian, Sean V. APPLICANT: Simard, Jacques APPLICANT: Simard, Jacques APPLICANT: Simard, Jacques APPLICANT: Rommens, Johanna M. APPLICANT: Rommens, Johanna M. APPLICANT: Myriad Genetics, Inc. TITLE OF INVENTION: Gene and Paralog FILE REFERENCE: 2318-258 FILE REFERENCE: 2318-258 FILE REFERENCE: 2318-258 FILING DATE: 1998-11-05 FRIOR FILING DATE: 1999-11-05 FRIOR PRILING DATE: 1999-11-05 FRIOR PRILING DATE: 1999-11-05 FRIOR FILING DATE: 1999-11-05 FRIOR FILING DATE: 1999-11-05 FRIOR APPLICATION NUMBER: 09/434,382 FRIOR FILING DATE: 1999-11-05 FRIOR FRIOR DATE: 1999-11-05 FRIOR FRIOR DATE: 1999-11-05 FRIOR FRIOR DATE: 1999-11-05 FRIOR FRIOR DATE: 1999-11-05 FRIOR FRIOR DATE: 1999-11-05 FRIOR FRIOR DATE: 1999-11-05 FRIOR FRIOR DATE: 1999-11-05 FRIOR FRIOR DATE: 1999-11-05 FRIOR FRIOR DATE: 1999-11-05 FRIOR FRIOR DATE: 1999-11-05 FRIOR FRIOR DATE:	100 100 vative
70000011111111111111111111111111111111	TI 1 9-564-805-3 quence 3, Application US/(Lent No. 633403) NERL INFORMATION: PELICANT: Tavtigian, Sear PELICANT: Teng, David H.: PELICANT: Simard, Jacquee PELICANT: Simard, Jacquee PELICANT: Myriad Genetic ITLE OF INVENTION: Genetic ITLE OF INVENTION: Genetic ITLE OF INVENTION: Genetic ITLE OF INVENTION UMBER: ILL REFERENCE: 2318-258 URRENT FILING DATE: 1999-11 WHER APPLICATION NUMBER: RIOR FILING DATE: 1999-11 WHER OF SEQ ID NOS: 240 OFTOR FILING DATE: 1999-11 WHER OF SEQ ID NOS: 240 OFTOR FILING DATE: 1999-11 TYPE: DAA OFTOR FILING DATE: 1999-11 WHER OF SEQ ID NOS: 240 OFTOR FILING DATE: 1999-11 WHER OF SEQ ID NOS: 240 OFTOR FILING DATE: 1999-11 WHER OF SEQ ID NOS: 240 OFTOR FILING DATE: 1999-11 OFTOR FILING D	Query Match Best Local Similarity Matches 2958; Conser
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0 0 0 1 2 2 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	US-09-564-805-3 US-09-564-805-3 Sequence 3, Application US/095- Patent No. 633403 GENERAL INFORMATION: APPLICANT: Tartigian, Sean V APPLICANT: Tartigian, Sean V APPLICANT: Simard, Jacques APPLICANT: Romens, Johanna ITILE OF INVENTION: Chromoso; ITILE OF INVENTION: Chromoso; ITILE OF INVENTION: Chromoso; ITILE OF INVENTION: Chromoso; ITILE OF INVENTION: Chromoso; FILE REFERENCE: 2318-258 CURRENT FILING DATE: 1998-11-03 PRIOR APPLICATION NUMBER: US PRIOR APPLICATION NUMBER: US PRIOR FILING DATE: 1999-11-03 PRIOR FILING DATE: 1999-11-03 NUMBER OF SEQ ID NOS: 240 SOFTWARE: PatentIN Ver. 2.0 SOFTWARE: PATENTER:	Query Ma Best Loc Matches

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APPLICANT: Tavigian, Sean V.
APPLICANT: Tavigian, Jacques
APPLICANT: Rommens, Johanna M.
APPLICANT: Myriad Genetics, Inc.
ITILE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility
ITILE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility
ITILE OF INVENTION: Gene and a Paralog and Orthologous Genes
FILE REFERENCE: 2318-258
CURRENT APPLICATION NUMBER: US/09/564,805
FILE REPERIOR APPLICATION NUMBER: US 60/107,468
PRIOR APPLICATION NUMBER: US/4109/434,382
PRIOR FILING DATE: 1999-11-05
PRIOR APPLICATION NUMBER: 1999-11-05
SEQ ID NOS: 240
SEQ ID NOS: 240
SEQ ID NO 223
LENGTH: 2908
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ORGANISM: Pan troglodytes
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Patent No. 6333403
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GENERAL INFORMATION:

APPLICANT: Tavtigian, Sean V.

APPLICANT: Tavtigian, Jacques

APPLICANT: Rommens, Johanna M.

APPLICANT: Rommens, Johanna M.

APPLICANT: Rommens, Johanna M.

APPLICANT: Rommens, Johanna M.

TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility

TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes

TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes

TITLE OF INVENTION: Qene and a Paralog and Orthologous Genes

CURRENT APPLICATION NUMBER: US/09/564,805

CURRENT FILING DATE: 1998-11-06

PRIOR FILING DATE: 1998-11-06

PRIOR FILING DATE: 1999-11-05

PRIOR FILING DATE: 1999-11-05

NUMBER OF SEQ ID NOS: 240

SOFTWARE: PatentIN Ver. 2.0
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Pred. No. 0;
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Best Local Similarity 98.5%;
Matches 2863; Conservative
                      gorilla
             TYPE: DNA

ORGANISM: Gorilla gori:

FATURE:

NAME/KEY: CDS

LOCATION: (1)..(2478)

US-09-564-805-225
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Sequence 1, Application US/09564805; Patent No. 633403; GENERAL INFORMATION: APPLICANT: Teng, David H.F.; APPLICANT: Simard, Jacques; APPLICANT: Rommens, Johanna M.

RESULT 4 US-09-564-805-1

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APPLICANT: Myriad Genetics, Inc.
TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility
TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility
TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes
FILE REFERENCE: 2318-258
CURRENT PEPLICATION NUMBER: US/09/564,805
CURRENT FILING DATE: 2000-05-05
PRIOR FILING DATE: 1998-11-06
PRIOR FILING DATE: 1998-11-06
NUMBER OF SEQ ID NOS: 240
SOFTWARE: PALCHIN VOR: 2.0
SEQ ID NO 1
LENGTH: 2481
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83.9%; Score 2481; E
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2481; Conservative 0; Mismatches
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; LOCATION: (1)..(2478)
US-09-564-805-1
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Pred. No. 0;
0; Mismatches
                                          vuery Match 55.6%;
Best Local Similarity 81.6%;
Matches 1958; Conservative
; FEATURE:
; NAME/KEY: CDS
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OTHER INFORMATION: positions 22211 and 23879 is
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APPLICANT: Tavtigian, Sean V.
APPLICANT: Teng, David H.F.
APPLICANT: Sinard, Jacques
APPLICANT: Sinard, Jacques
APPLICANT: Rommens, Johanna M.
TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility
TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes
TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes
FILE REFERENCE: 2318-258
CURRENT APPLICATION NUMBER: US 60/107,468
PRIOR FILING DATE: 1998-11-06
PRIOR APPLICATION NUMBER: 09/434,382
PRIOR FILING DATE: 1999-11-06
PRIOR SEQ ID NOS: 240
NUMBER OF SEQ ID NOS: 240
SOFTWARE: PatentIN Ver. 2.0
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NAME/KEY: misc_feature
LOCATION: (910). (13104)
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LOCATION: (910). (13104)
CTHER INFORMATION: exon 1: 910-1154; exon 2: 1736-1786; exon 3:
CTHER INFORMATION: exon 6: 5582-5650; exon 7: 7075-7194; exon 8:
CTHER INFORMATION: 8186-8244; exon 9: 12878-12936; exon 10:
NAME/KEY: misc_feature
LOCATION: (13756). (122917)
CTHER INFORMATION: 13: 16278-16416; exon 12: 15283-15378; exon 17: 707ER INFORMATION: 133: 16278-16416; exon 14: 16499-16583; exon 15: 707HER INFORMATION: 133: 16278-16416; exon 14: 16499-16583; exon 17: 707HER INFORMATION: 2172-22310; exon 18: 22879-22917
NAME/KEY: misc_feature
LOCATION: (23045). (26452)
CTHER INFORMATION: 21: 22973-24093; exon 22: 24354-24432; exon 23: 707HER INFORMATION: 22: 22373-24093; exon 22: 24354-24432; exon 23: 707HER INFORMATION: 2502-25170; exon 22: 24354-24432; exon 23: 707HER INFORMATION: 2502-25170; exon 22: 24354-24432; exon 23: 707HER INFORMATION: 21: 22973-24093; exon 22: 24354-24432; exon 23: 707HER INFORMATION: 2502-25170; exon 22: 24354-24432; exon 23: 707HER INFORMATION: 2502-25170; exon 24: 25812-26036; polyadenylation CTHER INFORMATION: 18 to positions 1914, 5568, 7165, 16411, 1857 and 20486
CTHER INFORMATION: 18 C or T; n at position 13128 is t or tgat; r at
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Patent No. 6333403
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APPLICANT: Tavtiqi
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APPLICANT: Tratigian, Sean V.
APPLICANT: Teng, David H.F.
APPLICANT: Simard, Jacques
APPLICANT: Simard, Jacques
APPLICANT: Rommens, Johanna M.
APPLICANT: Myriad Genetics, Inc.
TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility
TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes
FILE REFRENCE: 2118-258
CURRENT APPLICATION NUMBER: US/09/564,805
CURRENT PRILING DATE: 2000-05-05
PRIOR PEPLICATION NUMBER: US 60/107,468
PRIOR FILING DATE: 1998-11-06
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                                                 Score 657.2; DB 4;
Pred. No. 9.6e-167;
0; Mismatches 3;
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Patent No. 6333403
                                                 22.2%;
99.5%;
                                                 Query Match
Best Local Similarity 99.5
Matches 659; Conservative
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; UTHEK INFORMED
US-09-564-805-28
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; Sequence 4, Application US/09564805; Patent No. 6333403
                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 98.0%;
Matches 301; Conservative 0
                                                                                                                                                                                                                                                    TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                ; NAME/KEY: CDS
; LOCATION: (51)..(293)
US-09-564-805-210
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                                                                                                                                                                                                                                                                 22.1%; Score 655; DB 4; Length 655; 100.0%; Pred. No. 5.2e-167; ive 0; Mismatches 0; Indels
PRIOR APPLICATION NUMBER: 09/434,382
PRIOR FILING DATE: 1999-11-05
NUMBER OF SEQ ID NOS: 240
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 27
LENGTH: 655
TYPE: DNA
CREAMISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 8
US-09-564-805-210
Sequence 210, Application US/09564805
Sequence 210, Application US/09564805
GENERAL INFORMATION:
APPLICANT: Tary San V.
APPLICANT: Application Sean V.
APPLICANT: Simard, Jacques
                                                                                                                                  FEATURE:

NAME/KEY: misc feature

LOCATION: (1). [228)

OTHER INFORMATION: exon 24

NAME/KEY: polyA signal

LOCATION: (536). (641)

US-09-564-805-27
                                                                                                                                                                                                                                                                                                   Matches 655; Conservative
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Best Local
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APPLICANT: Rommens, Johanna M.
APPLICANT: Myriad Genetics, Inc.
TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility
TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility
TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes
CURRENT APPLICATION NUMBER: US/09/564,805
CURRENT FILING DATE: 2000-05-05
PRIOR APPLICATION NUMBER: US 60/107,468
PRIOR APPLICATION NUMBER: 09/434,382
PRIOR FILING DATE: 1998-11-05
NUMBER OF SEQ ID NOS: 240
SOFTWARE PATENTING DATE: 1999-11-05
SOFTWARE PATENTING DATE: 1999-11-05
SOFTWARE PATENTING DATE: 1999-11-05
SEQ ID NO 210
LENGTH: 350
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APPLICANT: Tavtigian, Sean V.
APPLICANT: Tavtigian, Sean V.
APPLICANT: Tavtigian, Jacques.
APPLICANT: Simard, Jacques.
APPLICANT: Rommens, Johanna M.
APPLICANT: Rommens, Johanna M.
TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes
TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes
TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes
CURRENT FILING DATE: 2000-05-05
FILE REPERIOR: 1999-11-05
PRIOR PAPLICATION NUMBER: US 60/107,468
PRIOR FILING DATE: 1999-11-05
PRIOR FILING DATE: 1999-11-05
NUMBER OF SEQ ID NOS: 240
SOFTWARE: Patentin Ver. 2.0
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Pred. No. 9.9e-71;
0; Mismatches 6;
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; 0

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Sequence 26, Application US/09564805
; Patent No. 6333403
; GENURAL INFORMATION:
; APPLICANT: Tavtigian, Sean V.
; APPLICANT: Tavtigian, Sean V.
; APPLICANT: Simard, Johanna M.
; APPLICANT: Simard, Johanna M.
; APPLICANT: Myriad Genetics, Inc.
; TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility
; TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility
; TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility
; TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility
; TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility
; TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility
; TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility
; FILE REFERENCE: 2300-05-05
; CURRENT APPLICATION NUMBER: US/09/564,805
; CURRENT FILING DATE: 1998-11-06
; PRIOR APPLICATION NUMBER: 09/434,382
; PRIOR FILING DATE: 1999-11-05
; SOFTWARE: PATENT NOS: 240
; SOFTWARE: PATENT NOS: 240
; SOFTWARE: PATENT NOS: 240
; SOFTWARE: PATENT NOS: 240
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APPLICANT: Teng, David H.F.
APPLICANT: Simartd, Jacques
APPLICANT: Rommens, Johanna M.
APPLICANT: Myriad Genetics, Inc.
TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility
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                                                                                                                                                                       121 AGTTAAAGGTTGCTCGCCTGGACAACATATTCCTGACAAGGAATGCACTGGTCTAATGTTG 180
                                                                       61 AGTICAACCGGTATCICITCAACTGTGGAGAAGGCGTTCAGAGACTCATGCAGGAGCACA 120
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Pred. No. 7.7e-30;
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Patent No. 533403
GENERAL INFORMATION:
APPLICANT: Tavtigian, Sean V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc_feature

| LOCATION: (1)...(145)

| OTHER INFORMATION: exon 23

US-09-564-805-26
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                             RESULT 11
US-09-564-805-26
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APPLICANT: Ford, Donna M.
APPLICANT: Ford, Donna M.
APPLICANT: Levis, Marcia E.
APPLICANT: Schlegel, Robert
TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
TITLE OF INVENTION: PRODUCTS
FILE REPERENCE: CCC-257 (US)
CURRENT FILING DATE: 1999-06-08
EARLIER FILING DATE: 1998-06-10
NUMBER OF SEQ ID NOS: 850
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 315
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10.0%; Score 295; DB 4; Length 295;
Best Local Similarity 100.0%; Pred. No. 4e-70;
Matches 295; Conservative 0; Mismatches 0; Indels
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100.0%; Pred. No. 1.6e-54;
Live 0; Mismatches 0;
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Patent No. 6262333
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APPLICANT: Steinmann, Kathleen E.
APPLICANT: Astle, Jon H.
APPLICANT: Burgess, Christopher C.
APPLICANT: Bushnell, Steven E.
APPLICANT: Carroll III, Eddie
APPLICANT: Catino, Theodore J.
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Matches 237; Conservative
                                                                  FEATURE:
NAME/KEY: misc feature
LOCATION: (51)..(295)
OTHER INFORMATION: exon 1
                      TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Homo sapiens
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US-09-328-111-315
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LENGTH: 295
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US-09-564-805-4
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TYPE: DNA
ORGANISM: Homo sapiens
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US-09-564-805-10
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US-09-564-805-24
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APPLICANT: Tavigian, Sean V.
APPLICANT: Tavigian, Sean V.
APPLICANT: Tavigian, Sean V.
APPLICANT: Tavigian, Sean V.
APPLICANT: Tang, David H.F.
APPLICANT: Rommens, Johanna M.
APPLICANT: Myriad Genetics, Inc.
TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility
TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes
FILE REFERENCE: 2318-258
CURRENT APPLICATION NUMBER: US/09/564,805
CURRENT FILING DATE: 1999-11-06
PRIOR APPLICATION NUMBER: US 60/107,468
PRIOR APPLICATION NUMBER: 09/434,382
PRIOR FILING DATE: 1999-11-05
NUMBER OF SEQ ID NOS: 240
SEQ ID NO 20
SEQ ID NO 20
LENGTH: 139
MUCHARE AND ARTER OF SEQ ID NOS: 200
SEQ ID NO 20
LENGTH: 139
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           Gene and a Paralog and Orthologous Genes
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Best Local Similarity 100.0%; Pred. No. 3.1e-28;
Matches 139; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
4.7%; Score 139; DB 4; L
Best Local Similarity 100.0%; Pred. No. 3.1e-28;
Matches 139; Conservative 0; Mismatches 0;
                        FILE REFERENCE: 2318-258
CURRENT APPLICATION NUMBER: US/09/564,805
CURRENT FILING DATE: 2000-05-05
PRIOR PILING DATE: 1998-11-06
PRIOR FILING DATE: 1998-11-05
PRIOR FILING DATE: 1999-11-05
NUMBER OF SEQ ID NOS: 240
SOFTWARE: Patentin Ver: 2.0
LENGTH: 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 20, Application US/09564805; Patent No. 6333403
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| LOCATION: (1)...(139)

| OTHER INFORMATION: exon 17

US-09-564-805-20
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; OTHER INFORMATION: exon 13
US-09-564-805-16
                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc_feature
LOCATION: (1)..(139)
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             TITLE OF INVENTION:
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GENERAL INFORMATION:
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US-09-564-805-20
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Tavidian, Sean V.
APPLICANT: Tavidian, Hr.
APPLICANT: Rommens, Jacques
APPLICANT: Myriad Genetics, Inc.
TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility
TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes
TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes
TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes
TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes
TITLE OF INVENTION: Gene and a Paralog
FILE REFERENCE: 218-258
CURRENT FILING DATE: 1998-11-06
PRIOR APPLICATION NUMBER: US 60/107, 468
PRIOR APPLICATION NUMBER: US 99/34, 382
PRIOR FILING DATE: 1999-11-05
NUMBER OF SEQ ID NOS: 240
SEQ ID NO 24
LENGTH: 121
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Patent No. 633403
GENERAL INFORMATION; Sean V.
APPLICANT: Teng, David H.F.
APPLICANT: Simrad, Jacques
APPLICANT: Rommens, Johanna M.
APPLICANT: Myriad Genetics, Inc.
TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility
TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes
FILE REFERENCE: 2318-258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1959 TTTCAGACCTGTCTGGTGCGGCACTGCAAGCATGCGTTTGGCTGTGCGCTGGTGCACACC 2018
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                                                         61 TTACGGAGACCAGGTGGACAGGCTCCTGGCTGCTGCTGTTTTGTGTCCCACCT 120
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4.1%; Score 121; DB 4; Length 121;
Best Local Similarity 100.0%; Pred. No. 2.1e-23;
Matches 121; Conservative 0; Mismatches 0; Indels
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Patent No. 6333403
                                                                                                                                    1691 GCACGCAGATCACCACACG 1709
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| LOCATION: (1)...(121)

| CTHER INFORMATION: exon 21

US-09-564-805-24
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Search completed: May 18, 2003, 00:09:50 Job time: 249 secs

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Perfect score:

Sequence:

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Scoring table:

Minimum DB Maximum DB

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US SEQUENCE 3, Application US/0998626

PUBLICATION NO. US20030044959A1

GENERAL INFORMATION:

APPLICANT: Tautigian, Sean V.

APPLICANT: Tautigian, Sean V.

APPLICANT: Tautigian, Sean V.

APPLICANT: Simard, Jacques

APPLICANT: Rommens, Johanna M.

APPLICANT: Rommens, Johanna M.

APPLICANT: Myriad Genetics, Inc.

ITILE OF INVENTION: Groe and a Paralog and Orthologous Genes

TITLE OF INVENTION: UNUMBER: US/09/988,626

CURRENT APPLICATION NUMBER: 09/564,805

PRIOR APPLICATION NUMBER: 09/564,805

PRIOR APPLICATION NUMBER: 09/564,805

PRIOR PILING DATE: 1998-11-06

PRIOR PILING DATE: 1999-11-06

PRIOR PILING DATE: 1999-11-06

PRIOR PILING DATE: 1999-11-06

PRIOR PILING DATE: 1999-11-06

PRIOR PILING DATE: 1999-11-05

NUMBER OF SEQ ID NOS: 240

SOFTWARE: Patentin Ver. 2.0
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NAME/KEY: misc_feature
LOCATION: (51)...(2531)
LOCHTRR INSEMATION: coding sequence as in SEQ ID NO:1
US-09-988-626-3
                           US-09-988-626-26
US-09-988-626-26
US-09-988-626-16
US-09-988-687-16
US-09-988-687-20
US-09-988-687-20
US-09-988-687-20
US-09-988-687-20
US-09-988-626-11
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100.0%; Pred. No. 0;
ive 0; Mismatches
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Matches 2958; Conservative
                              TYPE: DNA ORGANISM: Homo sapiens
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Sequence 28, Appl
Sequence 27, Appl
Sequence 27, Appl
Sequence 2038, Ap
Sequence 2038, Ap
Sequence 2010, App
Sequence 210, App
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Sequence 223, Appli
Sequence 223, App
Sequence 225, App
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Sequence 21, Appli
Sequence 221, Appli
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                                                                                                      May 18, 2003, 00:09:53 ; Search time 359 Seconds (without alignments) 10628.516 Million cell updates/sec
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GENERAL INPORMATION:
APPLICANT: Tartigian, Sean V.
APPLICANT: Tartigian, Sean V.
APPLICANT: Targ, David H.F.
APPLICANT: Sharatd, Jacques
APPLICANT: Myriad Genetics, Inc.
TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility
TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes
FILE REFRENCE: 2318-258
CURRENT APPLICATION NUMBER: 105/09/988,687

CURRENT FILING DATE: 2001-11-20

PRIOR APPLICATION NUMBER: 09/564,805

PRIOR APPLICATION NUMBER: 09/564,805

PRIOR APPLICATION NUMBER: 09/434,382

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NUMBER OF SEQ ID NOS: 240

SOFTWARE: PatentIN Ver. 2.0
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100.0%; Score 2958;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2958; Conservative 0; Mismatches
TYPE: DNA
ORGANISM: Homo sapiens
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APPLICANT: Tavitgian, Sean V.
APPLICANT: Teng, David H.F.
APPLICANT: Sinard, Jacques
APPLICANT: Sinard, Jacques
APPLICANT: Rommens, Johanna M.
APPLICANT: Rommens, Johanna M.
APPLICANT: Myriad Genetics, Inc.
TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Suscept.
TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Suscept.
TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Suscept.
TITLE OF INVENTION: Queen and a Paralog and Orthologous Genes
FILE REFERENCE: 2318-258
CURRENT APPLICATION NUMBER: US 09/998, 626
CURRENT FILING DATE: 2000-05-05
PRIOR FILING DATE: 1998-11-06
PRIOR APPLICATION NUMBER: 09/434,382
PRIOR FILING DATE: 1999-11-05
PRIOR APPLICATION NUMBER: 09/434,382
PRIOR FILING DATE: 1999-11-05
SOFTWARE: Patentin Ver. 2.0
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ilarity 99.3%;
Conservative (
                                                                                                                                                                                                                                                                     TYPE: DNA ORGANISM: Pan troglodytes
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Best Local Similarity
Matches 2887; Conserv
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; LOCATION: (1)
US-09-988-626-223
                                                                                                                                                                                                                                             Q ID NO 223
LENGTH: 2908
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Sequence 223, Application US/09988687

Sequence 223, Application No. US20030045704A1

GENERAL INFORMATION:
APPLICANT: Tarvigian, Sanar V.
APPLICANT: Teng, David H.F.
APPLICANT: Simard, Jacques
APPLICANT: Simard, Jacques
APPLICANT: Myriad Genetics. Inc.
TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility
TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes
TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes
CURRENT FILING DATE: 2318-258
CURRENT FILING DATE: 2000-05-05
PRIOR APPLICATION NUMBER: US 60/107,468
PRIOR FILING DATE: 1999-11-05
PRIOR FILING DATE: 1999-11-05
PRIOR FILING DATE: 1999-11-05
SOFTWARE: PALCATION NUMBER: 09/434,382
PRIOR FILING DATE: 1999-11-05
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SOFTWARE: PALCATION NUMBER: 09/434,382
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Best Local Similarity 99.3%;
Matches 2887; Conservative (
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, NAME/KEY: CDS

, LOCATION: (1) ...

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                                CCCAACCAGCTCAAAGCCTGGCTCCAGCAGTACCACAACCAGTGCCAGGAGGTCCTGCAC
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Publication No. US20030044959A1

GENERAL INFORMATION:

APPLICANT: Tavtigian, Sean V.

APPLICANT: Tavtigian, Sean V.

APPLICANT: Simard, Jacques

APPLICANT: Somens, Johanna M.

APPLICANT: Myriad Genetics, Inc.

TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility

TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes

FILE REFERENCE: 2318-258

CURRENT APPLICATION NUMBER: US/09/988,626

FRICH REPLIANT FILING DATE: 2001-11-20

PRIOR FILING DATE: 1999-11-06

PRIOR FILING DATE: 1999-11-06

PRIOR FILING DATE: 1999-11-05

NUMBER OF SEQ ID NOS: 240

SEQ ID NO 225

LENGTH: 2892

LENGTH: 2892
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ORGANISM: Gorilla gorilla
FEATURE:
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Sequence 225, Application US/09988687

Sequence 225, Application US/09988687

GENERAL INFORMATION:

APPLICANT: Tavigian, Sean V.

APPLICANT: Tavigian, Jacques

APPLICANT: Timed, Jacques

APPLICANT: Rommens, Johanna M.

TITLE OF INVENTION: Chromosome 170-Linked Prostate Cancer Susceptibility

TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes

FILE REFERENCE: 2318-258

CURRENT APPLICATION NUMBER: US/09/988,687

CURRENT PILING DATE: 2001-11-20

PRIOR APPLICATION NUMBER: 09/64,805

PRIOR APPLICATION NUMBER: 09/64,805

PRIOR PLILING DATE: 1998-11-06

PRIOR FILING DATE: 1998-11-06

PRIOR FILING DATE: 1999-11-05

NUMBER OF SEQ ID NOS: 240

SEQ ID NOS: 240

SEQ ID NOS: 250 2750 2744 2684 2804 CTGCCCCACGCACGCACCCGTATCTGCCCTCCTTGCTGGTAGAAGCTGAAGAGCACGGTC GCCGCCTCGGAGGATGGGGACCTCAGCAGAAACGGCCCCACACAGAGAGCACACAGGCC AAGAAGGTCAGAGCCCAGTGAAGATCTGGGAGACCCTGAATTCAGAAGGCTGTGTGTCTT CTGCCCCACGCACGCACCCGTATCTGCCCCTCCTTGCTGGTAGAAGCTGAAGAGCACGGTC CCCCAGGAGGCAGCTCAGGATAGGTGGTATGGAGCTGTGCCCGAGGCTTGGGCTCCCCACAT CCCCAGGAGGCAGCTCAGGATAGGTAGGTATGGAGCTGTGCCGAGGCTTAGGCTCCCACAT AAGCACTAGTCTATAGATGCCTCTTAGGACTGGTGCCTGGCACAGCCGCGGGCCAGGGGG Length 2892 ъ •-DB Score 2819.6; Pred. No. 0; 0; Mismatches TCAGCTGCAATAAAGATTGAGTTTGCAA 2958 2865 TCAGCTGCAATAAAGATTGAGTTTGCAA 2892 95.3%; 98.5%; TYPE: DNA ORGANISM: Gorilla

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CGC 110 CGC 60 CGC 60 CTG 170 CTG 120 CTG 230 CTG 230	TC 290 	CC 410 	53 59 54	CA 650 CA 600 AT 710 AT 710 AT 660	77 77 72 72 83 83	IAC 890 	TC 1010 TC 960 TG 1070 TG 1020 TG 1130 GG 1130
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GGCGCTTTGCTGCTGCTGCGGGCCGGACGCACCATGTCGCAGGGACGGGCGCTTTGCTTGC	36CAGCGGGTAGCCGC 	AAGGTTGCTCGCACACATATTCCTGACACGAATGCACTGGTCTAATGTTGC AAGGTTGTTCGCCTGGACACATATTCCTGACACGAATGCACTGGTCTAATGTTGC TTAAGTGGAATGATTTCTTAAAGGAATGCACTGGTCTAATGTTGCTGGTTGCTTTGCTTGC	CCTCCACAACTGGAAAATACCTCGAAGCAATCAAAATATTTTCTGGTCCATTGAAAGGA 	CAGATCCCCATACACAGTGAACAGGAGGGAAAGCACCAACCA		GAGATGGGCCTCCCAGTTGGGACAGCTGCCATCGCTCCATTGCTGCTGTCAAGGAC GAGATGGGCCTCCCAGTTGGGACAGCTGCCTCCCATCATTGCTGCTGTTCAAGGAC GGGAAAAGCATCACTTGAAGGACAGAGTTTTTGGCTGAAGACTGCTCCTCCCCCCCC	GATCCTGGTGCTGCTTTTGTGGTGGTAGAATGTCCAGATGAAAGCTTCATCAACCCATC
ATGTGGG ATGTGGGG ACCATAT ACCATGC CGCACGC CGCACGC	CAGGTGGTC	AAGGTTG AAGGTTG TTAAGTG	CCTCCAC CCTCCAC ATAGAAC	TACCAGAT TACCAGAT GAAAGGCC GAAAGGCC	GAGCCAC GAGCCAC GTAGCTT 	GAGATGG GAGAAAA 	GATCCTG
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8 8	1251	ACCOSTITICGETTTAMAGAGAGAGACCCCCCCCCCCCCCTCCCTCCCTCCCTCCCT
QQ	1201	ACCAGTITICCCCTGTAAGAAGGAGGCCCCACCCTCAGTGTTCTTTTTTTT
ò	1311	TGCCTCCTCAAGTACCAGCTCCCACGAGGGAGGGAGAGGGATGCCATTATTACT 1370
g ò	1261	TGCCTCCTCCTCAAGTACCAGCTCCGTCCCAGGAGGGAATGGCAGAGGGATGCCATTATCACT 1320 TGCAATCCTGAGGAATTCATAGTTGAGGCGCTGCAGCTTCCCAACTTCCAGCAGAGGGTG 1430
G Q	1321	
ð i	1431	CAGGAGTACAGGAGGAGTGCGCAGGACGGCCCAGCAGCAGAAAAAAAA
3 8	1491	CCAGAAATCATCCTTCGAACAGGGTCTGCCATCCGATGAAGATTCGAAATGTCAGT 1550
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٥٧	1551	GCCACACTTGTCAACATAAGCCCCGACACGTCTCTGCTACTGGACTGTGGGGGACA 1610
qq	1501	GCCACACTTGTCAACATAAGCCCCGACACGTCTCTGCTACTGGACTGTGGTGAGGGCACG 1560
ઠે ત	1611	TITGGGCAGCTGTGCCGTCATTACGGAGACCAGGTGGACAGGGTCCTGGGCACCCTGGCT 1670
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à 8	1671	GCTGTTTGTGTTCCACCTGCACCCAGATCACCACACGGGCTTGCCAAAATATCTTGCTG 1/30 GCTGTGTTTGTGTCCCACCTGCACGAGATCACCACGGGGCTTGCTAAATATCTTGCTG 1680
δ	1731	CAGAGAGAACGCGCCTTGGCATCTTTGGGAAAGCCGCTTCACCCTTTGCTGGTGGTTGCC 1790
QΩ	1681	CAGAGAGAACATGCTTGGCATCTTTGGGAAAGCCCCTTCACCCTTTGCTGGTGGTTGCT 1740
ò	1791	CCCAACCAGCTCAAAGCCTGGCTCCAGCAGTACCACAAGTGCCAGGAGGTCCTGCAC 1850
QQ	1741	CCCAGCCAGCTCAAAGCCTGGCTCCAGCAGTACCACAACCAGTGCCAGGAGGTCCTGCAC 1800
δλ	1851	CACATCACTATGATTCCTGCCAAATGCCTTCAGGAAGGGGCTGAGATCTCCAGTCCTGCA 1910
QQ	1801	CACATCAGTATGATTCCTGCCAAATGCCTTCAGGAAGGGGCTGAGATCTCCAGTCCTGCA 1860
Ş E	1911	GTGGAAGATTGATCAGTTCGCTGTTGCGAACATGTGATTTGGAAGAGTTTCAGACCTGT 1970
3 8	1971	CTGGTGCGCACTGCAAGCATGCGTTTGGCTGTGCGCTGGTGCACACCTCTGGCTGG
qq	1921	CTGGTGCGGCACTGCAAGCATGCGTTTGGCTGTGCGCTGGTGCACCTCTGGCTGG
ò	2031	GTGGTCTATTCCGGGGACACCATGCCCTGCGAGGCTCTGGTCCGGATGGGGAAGATGCC 2090
qq	1981	GIGGTCTAITCCGGGGACACCATGCCCTGCGAGGCTCTGGTCCGCATGGGGAAAGATGCC 2040
ογ	2091	ACCTCCTGATACATGAAGCCACCCTGGAAGATGCTTTGGAAGAGGAAGCAGTGGAAAAG 2150
qq	2041	accercerearacareaeceaecereeaaeareerrreeaaeaecaereeaaaae 2100
δλ		ACACACAGCACAACGTCCCAAGCCATCAGCGTGGGGGATGCGGATGAACGCGGAGTTCATT 2210
qq		ACACACAGGCACAAGGCCCAAGCCATCAGGGGGATGGGGGATGAACGCGGAGTTCATT 2160
ò	2211	ATGCTGAACCACTTCAGCCAGCGCTATGCCAAGGTCCCCCTTTCAGCCCCCAACTTCAGC 2270

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NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin Ver.
SEQ ID NO 1
LENGTH: 2481
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ORGANISM: Homo
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Publication No US20030044959A1

GENERAL INROMATION:

APPLICANT: Tartigian, Sean V.

APPLICANT: Tartigian, Sean V.

APPLICANT: Tartigian, Sean V.

APPLICANT: APPLICANT: Acques

APPLICANT: Myriad Genetics, Inc.

ITILE OF INVENTION: Gheetics, Inc.

TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes

FILE REFRENCE: 2318-258

CURRENT APPLICATION NUMBER: US/09/988,626

CURRENT FILING DATE: 2001-11-20

PRIOR FILING DATE: 2000-05-05

PRIOR FILING DATE: 1998-11-06

PRIOR FILING DATE: 1998-11-05

PRIOR FILING DATE: 1999-11-05
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Best Local Similarity 100.
Matches 2481; Conservative
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; NAME/KEY: CDS
; LOCATION: (1)..(2478)
US-09-988-626-1
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Sequence 1, Application US/09988687

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GENERAL INFORMATION:
APPLICANT: Targ, David H.F.
APPLICANT: Simard, Jacques
APPLICANT: Rowmens, Johanna N.
APPLICANT: Myriad Genetics, Inc.
TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility
TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes
FILE REFERENCE: 2318-258

CURRENT APPLICATION NUMBER: US/09/988,687

CURRENT FILING DATE: 2000-11-20

PRIOR APPLICATION NUMBER: US 60/107,468

PRIOR PILING DATE: 1999-11-05

PRIOR FILING DATE: 1999-11-05

PRIOR FILING DATE: 1999-11-05

WUMBER OF SEQ ID NOS: 240

SEQ ID NO 1

LENGTH: 2481

THENDEL TARGET OF THE OF T 2330 2390 2450 2460 Gaps 2041 ACCCTCCTGATACATGAAGCCACCCTGGAAGATGGTTTGGAAGAGGAAGAGGAAGTGGAAAAG GAGAAAGTGGGAGTTGCCTTTGACCACATGAAGGTCTGCTTTGGAGACTTTCCAACAATG GAGAAAGTGGGAGTTGCCTTTGACCACATGAAGGTCTGCTTTGGAGACTTTCCAACAATG CCCAAGCTGATTCCCCCCACTGAAAGCCCTGTTTGCTGGGGGGACATCGAGGAGAAGGAG CGCAGGAGAAGCGGGAGCTGCGGGCAGGTGCGGGCGGCCCTCCTGTCCAGGGAGCTGGCA 1981 GTGGTCTATTCCGGGGACACCATGCCCTGCGAGGCTCTGGTCCGGATGGGGAAAGATGCC ATGCTGAACCACTTCAGCCAGCGCTATGCCAAGGTCCCCCTCTTCAGCCCCAACTTCAGC CGCAGGGAGAAGCGGGAGCTGCGGCAGGTGCGGGCCCCTCCTGTCCAGGGAGCTGGCA ACACACAGACAAACGTCCCAAGCCATCAGCGTGGGGATGCGGGATGAACGCGGGAGTTCATT ACACACAGGCACAACGTCCCCAAGGCGTGGGGATGCGGATGAACGCGGAGTCATT CCCAAGCTGATTCCCCCACTGAAAGCCCTGTTTGCTGGCGACATCGAGGAGATGGAGGAG <u> ACCCTCCTGATACATGAAGCCACCCTGGAAGATGGTTTGGAAGAGGAAGCAGTGGAAAAG</u> .. 0 Length 2481; Indels 0 ٠. م DB Query Match 83.9%; Score 2481; E Best Local Similarity 100.0%; Pred. No. 0; Matches 2481; Conservative 0; Mismatches 2461 AAGAAGGTCAGAGCCCAGTGA 2481 ORGANISM: Homo sapiens ; NAME/KEY: CDS ; LOCATION: (1)..(2478) US-09-988-687-1

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APPLICANT: Tartigian, Sean V.
APPLICANT: Tartigian, Sean V.
APPLICANT: Tartigian, Sacient M.F.
APPLICANT: Sinard, Jacques
APPLICANT: Romens, Jacques
APPLICANT: Romens, Jacques
APPLICANT: Romens, Johanna M.
APPLICANT: Myriad Genetics, Inc.
TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility
TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes
FILE REFERENCE: 2318-258
CURRENT APPLICATION NUMBER: US/09/988,626
CURRENT FILING DATE: 2000-06-05
PRIOR FILING DATE: 2000-06-05
PRIOR FILING DATE: 1998-11-06
PRIOR FILING DATE: 1998-11-06
PRIOR FILING DATE: 1998-11-06
SPRIOR FILING DATE: 1999-11-05
NUMBER OF SEQ ID NOS: 240
SEQ ID NO 221
LENGTH:: 2470
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Pred. No. 0;
0; Mismatches
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; Publication No. US20030044959A1
; GENERAL INFORMATION:
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US-09-988-626-221
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Publication No. US20030045704A1
GENERAL INFORMATION:
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Best Local Similarity 81.6%;
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APPLICANT: Taviijan, Sean V.
APPLICANT: Taviijan, Sean V.
APPLICANT: Taviijan, Sean V.
APPLICANT: Taviijan, Sean V.
APPLICANT: Taviijan, Saques
APPLICANT: Simard, Joaques
APPLICANT: Myriad Genetics, Inc.
ITILE OF INVENTION: Chromosome 179-Linked Prostate Cancer Susceptibility
ITILE OF INVENTION: Gene and a Paralog and Orthologous Genes
ITILE OF INVENTION: Gene and a Paralog and Orthologous Genes
ITILE OF INVENTION: Gene and a Paralog and Orthologous Genes
ITILE REPERENCE: 2318-258
CURRENT APPLICATION NUMBER: US/09/988,687
FILE REPERENCE: 2000-05-56
PRIOR PILING DATE: 1090-11-05
PRIOR PILING DATE: 1999-11-05
PRIOR PILING DATE: 1999-11-05
PRIOR PILING DATE: 1999-11-05
SOFTWARE: Patentin Ver: 2.0
SOFTWARE: Patentin Ver: 2.0
SEQ ID NO 221
LENGTH: 2470 647 Gaps CTGCGCACGCGAGAGAGCGCGGACCGTCGGGGTGCTCCGGCGGCCCAAACACGCGTGTAC 227 creceracededadadececece----egerecedesesecesadadecererae 153 cracadardardadadadadadadadadadadadadardardrardrardrardada 213 TTCAACCGGTATCTCTTCAACTGTGGAGAAGGCGTTCAGAGACTCATGCAGGAGCACAAG 347 407 GGCTTAAGTGGAATGATTCTTACTTTAAAGGAAACCGGGCTTCCAAAGTGTGTACTTTCT 467 393 527 453 GGAATAGAACTGGCTGTGCGGCCCCACTCTGCCCCAGAATACGAGGATGAAACCATGACA 587 GGAATAGAACTGGCCGTGCGGCCTCACTCTGCACCAGAATACAAGGATGAGACCATGACT 513 CGCACCATGTCGCAGGGTTCGGCTCGTCGGCCGCGGCCCAAAGACCCACTGCGACAC 99 CTGCAGGTGGTGGCAGCGGGTAGCCGGGACTCGGGCGCCGCGCTCTACGTCTTCTCCGAG TACAACAGGTACCTTTTTAACTGCGGAGAAGGCGTCCAACGACTTATGCAGGAACACAAG GGACCTCCACAACTGGAAAATACCTCGAAGCAATCAAAAATATTTTCTGGTCCATTGAAA TTAAAGGTTGCTCGCCTGGACAACATATTCCTGACACGAATGCACTGGTCTAATGTTGGG GGACCACCACAGCTGGAGAATATCTAGAAGCAATCAAAATATTTTCTGGTCCATTGAAA GGGTTGTGTGGAATGATTTAACTTTAAAGGAAACCGGGCTTCCCCAAATGTGTTTCTGTCT 24; Length 2470 CGCACCATATCGCAGGCACCCGCCGCCGCGAGCGGCCGCGCAAGGACCCGCT Score 1645.6; DB 9; Length Pred. No. 0; 0; Mismatches 417; Indels

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CTGCAGAGAGACGCGCCTTGGCATCTTTGGGAAAGCCGCTTCACCCTTTGCTGGTGGTT
                1699 GCTCCTACCCAGCTCAGGGCCTGGCTGCAGCAGTATCACAACCACCAGCAGGAGATTCTG
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Patent No. US20020132090A1
GENERAL INFORMATION:
TITLE OF INVENTION: No. US20020132090A1e1
FILE REFERENCE: 5800-119
CURRENT APPLICATION NUMBER: US/09/833,381
CURRENT PELING DATE: 2001-04-11
PRIOR FILING DATE: 2000-02-29
NUMBER OF SEQ ID NOS: 2050
SOFTWARE: FastSEQ for Windows Version 3.0
SEQUENCE: 783
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ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
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APPLICANT: Rommens, Johanna M.
APPLICANT: Myriad Genetics, Inc.
TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility
TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility
TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes
FILE REFERENCE: 2318-258
CURRENT PAPLICATION NUMBER: US/09/988,626
CURRENT FILING DATE: 2001-11-20
PRIOR APPLICATION NUMBER: 09/564,805
PRIOR FILING DATE: 1998-11-06
PRIOR PAPLICATION NUMBER: 09/434,382
PRIOR PELING DATE: 1998-11-05
PRIOR FILING DATE: 1999-11-05
NUMBER OF SEQ ID NOS: 240
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NOS: 240
SEQ ID NOS: 2864
THENTH: 26664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
FRATURE:
FRATURE:
FRATURE:
FRATURE:
FORMATION: (910)..(13104)
OTHER INFORMATION: exon 1: 910-1154; exon 2: 1736-1786; exon 3:
OTHER INFORMATION: 9105-1995; exon 4: 3025-3089; exon 5: 4361-4418;
OTHER INFORMATION: 1925-1995; exon 4: 3025-3089; exon 5: 4361-4418;
OTHER INFORMATION: 8186-8244; exon 9: 12878-12936; exon 10:
OTHER INFORMATION: 13032-13104;
NAMMS/KEY: misc feature
LCCATION: (13756)..(2291).
OTHER INFORMATION: exon 11: 13756-13868; exon 12: 15283-15378; exon OTHER INFORMATION: 13: 16278-16416; exon 14: 16498-16583; exon 15: OTHER INFORMATION: 22172-22310; exon 16: 2049-20445; exon 17: OTHER INFORMATION: 22172-22310; exon 18: 22879-22917
NAMMS/KEY: misc feature
LCCATION: (22045)..(26452)
OTHER INFORMATION: exon 19: 23043-24045; exon 17: 0THER INFORMATION: exon 19: 23043-24432; exon 27: 23188 INFORMATION: exon 19: 23043-24403; exon 27: 23188 INFORMATION: exon 24: 25812-26036; polyadenylation OTHER INFORMATION: signal: 26447-26452
OTHER INFORMATION: signal: 26447-26452
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OTHER INFORMATION: so at positions 826 and 23180 is G or C; y at OTHER INFORMATION: positions 22211 and 23180 is A or G.
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Pred. No. 2e-196;
0; Mismatches 3; Indels
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Best Local Similarity 99.5%;
Matches 659; Conservative (
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                                                                                                                       Length
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                                                                                                                 Score 734.8; DB 10;
Pred. No. 6.7e-222;
0; Mismatches 10;
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US-09-988-626-28
US-09-988-626-28
Sequence 28, Application US/09988626
Publication No. US20030044959A1
GENERAL INFORMATION:
APPLICANT: Tavtigian, Sean V.
APPLICANT: Tavtigian, Sean V.
APPLICANT: Simard, Jacques
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                                       or
                                                                                                                 Query Match
Best Local Similarity 98.3%;
Matches 772; Conservative
                                    = A,T,C
        ; LOCATION: (1)...(783)
; OTHER INFORMATION: n
US-09-833-381-2039
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TYPE: UNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: misc feature

LOCATION: (910). (13104)

OTHER INFORMATION: exon 1: 910-1154; exon 2: 1736-1786; exon 3:

OTHER INFORMATION: 1925-1995; exon 4: 3025-3089; exon 5: 4361-4418;

OTHER INFORMATION: 8186-8244; exon 7: 7075-7194; exon 8:

OTHER INFORMATION: 13032-13104;

OTHER INFORMATION: 13032-13104;

NAME/KEY: misc feature

LOCATION: (13756). (22977)

OTHER INFORMATION: 13: 16278-16416; exon 12: 15283-15378; exon 15:

OTHER INFORMATION: 13: 16278-16416; exon 14: 16498-16583; exon 15:

OTHER INFORMATION: 13: 16278-16416; exon 18: 22879-22917

NAME/KEY: misc feature

LOCATION: (23045). (26452)

OTHER INFORMATION: 23172-22310; exon 18: 22879-22917

NAME/KEY: misc feature

LOCATION: (23045). (26452)

OTHER INFORMATION: exon 19: 23045-23154; exon 20: 23795-23895; exon 31: 20THER INFORMATION: 21: 23973-24093; exon 22: 24354-24432; exon 23: 30THER INFORMATION: 22: 24354-24432; exon 23:
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 CCCTCCTTGCTGGTAGAAGCTGAAGAGCACGGTCCCCCAGGAGGCAGCTCAGGATAGGTG 26164
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and Orthologous Genes
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APPLICANT: Tavtigian, Sean V.
APPLICANT: Tavtigian, Sean V.
APPLICANT: Teng, David H.F.
APPLICANT: Simard, Jacques
APPLICANT: Rommens, Joaques
TITLEON: Simard, Chromosome Inp-Linked Pro-
TITLE OF INVENTION: Gene and a Paralog and O
FILE REFERENCE: 2318-258
CURRENT APPLICATION NUMBER: US/09/988,687
CURRENT FILING DATE: 2001-11-20
PRIOR PILING DATE: 2001-11-20
PRIOR PILING DATE: 1000-05.05
PRIOR PILING DATE: 1998-11-05
PRIOR FILING DATE: 1998-11-05
PRIOR FILING DATE: 1998-11-05
NUMBER OF SEQ ID NOS: 240
SOFTWARE: Patentin Ver: 2.0
SOFTWARE: Patentin Ver: 2.0
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US-09-988-687-28
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Publication No. US20030044959A1
GENERAL INFORMATION:
APPLICANT: Teng, David H.F.
APPLICANT: Simard, Jacques
APPLICANT: Romens, Johanna M.
APPLICANT: Romens, Johanna M.
APPLICANT: Myriad Genetics, Inc.
TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility
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MAME/KEY: variation
LOCATION: (826)...(23879)
COTHER INFORMATION: sat positions 826 and 23180 is G or C; y at OTHER INFORMATION: positions 1914, 5568, 7165, 16431, 1857 and 20486
OTHER INFORMATION: positions 1914, 5568, 7165, 16431, 1857 and 20486
OTHER INFORMATION: is C or T; n at position 13128 is t or tgat; r at US-09-988-687-28
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Sequence 27, Application US/09988687
Publication No. US20030045704A1
GENERAL INFORMATION:
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Matches 655; Conservative
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LOCATION: (1)...(228)
OTHER INFORMATION: exon
                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Homo sapiens
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; LOCATION: (636)..(641)
US-09-988-687-27
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100.0%; Pred. No. 1.1e-196;
iive 0; Mismatches 0;
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NAME/KEY: misc_feature

LOCATION: (1). [228)

OTHER INFORMATION: exon 24

NAME/KEY: polyA_signal

LOCATION: (536). (641)

US-09-988-626-27
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Best Local Similarity 100.(
Matches 655; Conservative
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ORGANISM: Homo sapiens
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APPLICANT: Tavtiglan, Sean V.
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APPLICANT: Tavtiglan, Sean V.
APPLICANT: Tavtiglan, Sean V.
APPLICANT: Simard, Joaques
APPLICANT: Rommens, Johanna M.
APPLICANT: Rommens, Johanna M.
APPLICANT: Myriad Genetics, Inc.
TITLE OF INVENTION: Cene and a Paralog and Orthologous Genes
FILE REFERENCE: 2318-258
CURRENT APPLICATION NUMBER: US/09/988,687
CURRENT FILING DATE: 2001-11-20
PRIOR APPLICATION NUMBER: 09/564,805
PRIOR APPLICATION NUMBER: 09/564,805
PRIOR APPLICATION NUMBER: 09/544,805
PRIOR PILING DATE: 1990-11-06
PRIOR FILING DATE: 1999-11-06
PRIOR FILING DATE: 1999-11-06
PRIOR PELING DATE: 1999-11-05
NUMBER OF SEQ ID NOS: 240
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Search completed: May 18, 2003, 02:19:09 Job time: 522 secs

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May 17, 2003, 15:56:54; Search time 6428.12 Seconds (without alignments) 11232.524 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Length DB ID Description	2908 9 AF304370 Homo sa	00.0 2992 6 AX405825 AX405825 Sequenc	.9 2997 9 BC001939 BC001939 Homo	.y 3006 y BC004158 BC004158 HOMO SA 3006 y BC004158 HOMO SA	7 2976 9 AK001392 AK001392 Homo sa	.5 2893 9 AF308694 AF308694 Gorilla	./ 2907 9 AKU94687 3 2734 9 AKU94333	.1 2163 9 AK074244 Homo	.0 2712 10 AF308696 AF308696 Mus	.2 2/93 9 AKU94012 AKU94012 HOMO	.3 679 9 HSA329331 AJ329331	.9 740 9 AF304371S2 AF304369 Homo	.8 34593 10 AF348157 Arsa AF348157 Mus 8 196566 10 AF663045 Arsa	.5 167336 2 AC128361 AC128361 Rattus	.5 186836 2 AC097911 AC097911	.4 2728 3 AY119279 .	.4 115873 2 AC017383 AC017383	.4 175681 3 AC007417 AC007417 .4 190574 2 AC007352 AC007352	.4 240481 3 AE003830 AE003830	.3 186836 2 AC097911 AC097911	.0 721 9 AF304371S1 .6 167336 2 AC128361	.3 2704 8 AY117303 AY117303	.3 2818 8 AY070061	.8 752 9 HSA329367 AJ329367 .6 1617 8 AY086950 AY086950	.4 31201 8 SPACID4 Z69239 S.pombe		.7 32329 8 SPBC3D6 Z95620 S.pombe	.6 143209 8 AP001550 AP001550 Oryza	.6 125020 9 AF429315	.4 75289 8 AB023046 Arabi	.4 2517 6 AR137565 AR137565	.4 251/ 6 AKL390/1 AKL390/1 Sequence	.4 .3685 8 SCIKKU/9C	.3 23533 1 AE001039 Archaeog	ALIGNMENTS	370 sapiens puta	170 170 170 GI:1088093		sablens.
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Submitted (12-SEP-2000) Myriad Genetics, Inc., 320 Wakara Way, Salt Lake City, UT 84108, USA Location/Qualifiers
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Desrochers, M., Dumont, M., Farnham, J.M., Frank, D., Frye, C.,
Ghaffari, S., Gupte, J.S., Hu, R., Iliev, D., Janecki, T., Kort, E.N.,
Ladity, K.E., Leavitt, A., Leblanc, G., McArthur-Morrison, J.,
Pederson, A., Penn, B., Peterson, K.T., Reid, J.E., Richards, S.
Schroeder, M., Smith, R., Snyder, S.C., Swedlund, B., Swensen, J.,
Thomas, A., Tranchant, M., Woodland, A.M., Labrie, F., Skolnick, M.H.,
Neuhausen, S., Rommens, J. and Cannon-Albright, L.A.
A candidate prostate cancer susceptibility gene at chromosome 17p
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AX405825
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Tang, Y.T., Liu, C., Zhou, P., Asundi, V., Zhang, J., Zhao, Q.A., Ren, F., Xue, A.J., Yang, Y., Wehrman, T. and Drmanac, R.T.
Novel nucleic acids and polypeptides
Patent: WO 0222660-A 240 21-MAR-2002;
HYSEQ, INC. (US) PAT 14-JUN-2002 Vertebrata; Euteleostomi; Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Eutele Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo

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	61 TTAAGTGGAATGATTCTTATAAGGAAACCGGGCTTCCAAAGTGTGTACTTTCTGGA 420 	CTTCCACAACTGGAAAATACCTCGAAGCAATCAAAATATTTTCTGGTCCATTGAAAGGA 480 	BI ATAGAACTGGCTGTGCGGCCCCACTCTGCCCCAGAATACGAGGATGAAACCATGACAGTT 540	141 TACCAGATCCCCATACACAGAGAGAGAGAGAAAGCACCAACCA	001 GAAAGGCCTCTCAGCAGCCTCAGTCCAGAGCGATCTTCAGACTCCGAGTCGAATGAAAAT 660 	i61 GAGCCACCTTCCACATGGTGTTAGCCAGAGAGGGGTCAGGGACTCTTCCCTGGTC 720 	21 GTAGCTITCATCTGTAAGCTTCACTTAAAGAGGAAACTTCTTGGTGCTCAAAGCAAAG 780 	BORGATGGGCCTCCCAGTTGGGACAGCTGCCATCGCTCCCATCATTGCTGCTGTCAAGGAC 840	141 GGGAAAAGCATCACTCATGAAGGAAGAGATTTTGGCTGAAGAGCTGTGTACTCCTCCA 900 	001 GATCCTGGTGCTGCTGGTGGTGGTAGAATGTCCAGATGAAAGCTTCATTCA	161 IGTGAGAATGCCACCTTTCAGAGGTACCAAGGAAAGGCAGATGCCCCGTGGCCTTGGTG 1020	021 GTTCACATGGCCCCAGCATCTGTGCTTGTGGACAGCTACCAGCAGTGGATGGA	111 TITGGGCCTGACACCTTGGTCCTGAATGAGAACTGTGCCTCAGTTCACAACCTT 1140	.41 GGCAGCCACAAGATTCAAACCCAGCTCAACCTCACCAGGACATCTTCCCCCTGCTC 1200 	101 ACCAGTITCGGCTGTAAGAAGGAGGCCCCACCCTCAGTGTGCCCATGGTTCAGGGTGAA 1260	161 TGCCTCCTCAAGTACCAGCTCCGTCCCAGGAGGAGTGGCAGGATGCCATTATTACT 1320	121 TGCAATCCTGAGGAATTCATAGTTGAGGGGCTGCAGCTTCCCAACTTCCAGCAGCGTG 1380
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RRDPSGGGGGORTUTLQVVAGSRDSGAALVYDESPRNATLFNGGGGVGLMQERKLKV
RRLDNIFLTRAHWSWUGGLGGMILTLKETGLPKCVLSGPPQLEKYLEAIKIRSGPLKG
IELAVRPHSAPEYEDETMTVYQIPIHSEQRRGKHQPWQSPERPLSRLSPERSSDSELN
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AVKDCKSITHEGREILAEELCTPPDPCAAFVVVECPDESFIQPICENATFQRYQGKAD
APVALVVHMAPASVLVDSRYQQMMERFGPDTQHLVLNBNCASVHNLRSHKIQTQLNLI
HPDIFPLLTSPRCKKEGPTLSVPWQCSCLLKYQLRPREWQDAIITCNPEFIVEA
LQLPNPQSVQEYRESAQDGPAPAEKRSQYPEIIFLGTGSAIPMKIRNVSATLVNISP
DTSLLLDCGEGTFGQLCRHYGDQVDRVLGTLAAVFVSHLHADHHTGLPSILLQRERAL
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|Sproduce="putative prostate cancer susceptibility protein"
|Protein_id="AAH01939.1"
|db_xref="GI:LS804973"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield, Susanna Chan, Readman Chiu, Chris Fjell, Brin Garland, Ran Guin, Letticia Haiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline Schelin, Duane Smailus, Michael Smith, Lorraine Spence, Jeff Scott, Miranada Tsai, Natasja van den Bosch, Jill Vardy, George Yang, Scott Zuyderduyn, Marco Marra.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Clone distribution: MGC clone distribution information can be foun through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAL Plate: 9 Row: i Column: 17
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 7022621.
Location/Qualifiers
                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

    (bases 1 to 2997)

                                                                                                                                                                                                                                                                                                                                                                                            Submitted (29-JAN-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                        protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
mail: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTP/DTP
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
BC Cancer Agencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
info@bcgsc.bc.ca
                                                                                                                                    BC001939 2997 bp mRNA linear PR Homo sapiens, putative prostate cancer susceptibility clone MGC:4102 IMAGE:2820640, mRNA, complete cds.
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/Lone_lib="NIH MGC_7"
/lab_host="DH10B-R"
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                    2535 AAGAAGGTCAGAGCCCAGTGA: 2555
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BC001939.1 GI:12804972
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KEYWORDS
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ASLGKPLHPLLVVAPNQLKAWLQQYHNQCQEVLHHISMIPAKCLQEGAEISSPAVERL
LISSLLRTCDLEEEYQTCLVRHCKHAFCALVHTSGWKVVYSGDTWPCEALVRWGKDATL
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GTGGTCTATTCCGGGGGACACCATGCCCTGCGAGGCTCTGGTCCGGATGGGGAAAGATGCC 2100 ACCCTCCTCATACATGAGCCACCCTGGAAGATGGTTTGGAAGAGGAAGCAGTGGAAAAG 2100 ACCCTCCTCATACATGAGCCACCCTGGAAGATGGTTTGGAAGGGAAGCAGTGGAAAAG 2160 ACCCTCCTCGAACACCTCCCAAGCCACCAGGGGGAAGCAGTGGAAAAG 2160 ACCCTCCTCGAACACCTCCCAAGCTCCCAAGTTGGAAGCAGTGGAAAAG 2160 ACCTCCTCGAACACCTCCCAAGCTCCCAAGTTGGAAGCAGTGGAACTTCAT 220 ATGCTGAACCACTTCAGCCAGCGCTATGCCAAGGTCCCCTCTTCAGCCCCAACTTCAGC 220 ATGCTGAACCACTTCAGCCAGGCTATGCCAAGGTCCCCCTCTTCAGCCCCAACTTCAGC 220 ATGCTGAACCACTTCAGCCAGGCTATGCCAAGGTCCCCCTCTTCAGCCCCAACTTCAGC 220 ATGCTGAACCACTTCAGCCAGGCTATGCCAAGGTCCCCCTCTTCAGCCCCAACTTCAGC 220 ATGCTGAACCACTTCAGCCAGGCTTTGGCAGGTCCCCTCTTCAGCCCCAACTTCAGC 220 ATGCTGAACCACTTCAGCCAGTGCAGGTCCCCCTCTTTCAGCCCCCAACTTCAGC 220 ATGCTGAACCACTTTGACCACTGAAGGTCCCCCTCTTTTGGAGACTTTCCCAACAATG 2340 ATGCTGAACCACTTTGACCACTGAAGGTCCTGCTTTTGGAGACTTTCCCAACAATG 2340 ATGCTGAACCACTGAAAGCCCTGTTTTGCTGGCGACATTTCCAACAATG 2340 ATGCTGAATCCCCCACTGAAAGCCCTGTTTTGCTGGCGACACTTCCAGGAGATGGAGGG 2400 ATGCTGAAGCTGCGGCAGGTCCGGCCACACTCCAGGGAGCTGGCA 2400 ATGCTGAACAAGCCTCTTTTGCTGGCGACCACTCCAGGGAGCTGGCA 2400 ATGCTGAACAAGCCCTGTTTTGCTGGCGACCTCCTGTCCCAGGGAGCTGGCA 2400 ATGCTGAACAAGCCCTGTTTTGCTGGCGACCTCCTGTCCCAGGGAGCTGGCA 2400 ATGCTGAACAAGCCCTGTTTTGCTGGCGACCCTCCTGTCCCAGGGAGCTGGCA 2400 ATGCTGAACAAGCCCTGTTTTGCTGGCGACCCTCCTCCCAGGGAGCTGGCA 2400 ATGCTGAACAAGCCCTGTTTTGCTGGCGACCCCCCCTGTCCCAGGGAGCTGCCCCCCCC	AAGAAGGTCAGAGCCCAGTGA AAGAAGGTCAGAGCCCAGTGA BC004158 Homo sapiens, putati Clone MGC:2441 IMAGE BC004158 I GI:13278 MGC.		NIH-MGC Project URL: http://mgc.nci.nih.gov Contact: MGC help desk Email: cgapbs-r@mail.nih.gov Tissue Procurement: DCTD/DTP CDNA Library Preparation: Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL) DNA Sequencing by: Institute for Systems Biology http://www.systemsbiology.org contact: amadan@systemsbiology.org Anup Madan, Rachel Dickhoff, Jessica Fahey, Stephanie Ford, Julia Greene, Mark Ketteman and Anuradha Madan	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAL Plate: 2 Row: c Column: 13 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 7022621. Location/Qualifiers 13006
Db 2041 Oy 2041 Db 2101 Oy 2161 Oy 2221 Oy 2221 Oy 2281 Oy 2281 Oy 2341 Oy 2341 Oy 2401 Oy 2401	SUL 0004 CUS FIN FIN FIN	SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL	REMARK COMMENT	FEATURES SOURCE
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	1381 CAGGAGTACAGGAGGCCCAGCCCAGCCCAGCAGAAAAGAAGTCAGTAC 1440	1561 TTTGGGCAGCTGTGCCGTGAGACCAGGTGGACAGGGTCCTGGGCACCTGGCT 1620	U-U 4-4 E-E	
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/organism="Homo sapiens"
| Da xref="Locuslo:6658"
| Ab xref="Locuslo:6658"
| Alone="MGC:2441 IMAGE:2820640"
| Alssue Fype="Lung, small cell carcinoma"
| Alone_lib="NIH MGC_7"
| Alobese="DHOB-R"
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llarity 99.4%; Pred. No. 0;
Conservative 0; Mismatches 16;
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Tavtigian, S.V., Simard, J., Teng, D.H.F., Abtin, V., Baumgard, M., Beck, A., Camp, N.J., Carillo, A.R., Chen, Y., Dayananth, P., Desrochers, M., Dumont, M., Farnham, J.M., Frank, D., Frye, C.,
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                       CAGAGAGAACGCGCCTTGGCATCTTTGGGAAAGCCGCTTCACCCTTTGCTGGTGGTTGCC
                                                                                                                 CCCAACCAGCTCAAAGCCTGGCTCCAGTACCACAGTGCCAGGAGGTCCTGCAC
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CAGAGAGAACGCGCCTTGGCATCTTTGGGAAAGCCGCTTCACCCTTTGCTGGTGGTTGCC
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Uppublished Journal Land Company C A candidate prostate cancer susceptibility gene at chromosome 17p Nat. Genet. 27 (2), 172-180 (2001) Ghaffari,S., Gupte,J.S., Hu,R., Iliev,D., Janecki,T., Kort,E.N., Laity,K.E., Leavitt,A., Leblanc,G., McArthur-Morrison,J., Pederson,K.T., Reid,J.E., Richards,S., Schederson,M., Smith,R., Snyder,S.C., Swedlund,B., Swensen,J., Thomas,A., Tranchant,M., Woodland,A.M., Labrie,F., Skolnick,M.H., Neuhausen,S., Rommens,J., and Cannon-Albright,L.A. 61 ACCATATOGCAGGCACCCGCCGCGCGGGGCGCCGCGAAGGACCCGGTGCGGCACCTG 120 61 ACCATATCGCAGGCACCCGCCGCGCGGGGGCGCGCGAAGGACCCGCTGCGGCACCTG 120 Gaps 1 ATGTGGGCGCTTTGCTCGCTGCTGCTGCGGGCCGGACGCACCATGTCGCAGGGACGC 60 9 . Length 2908; Indels g

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REFERENCE AUTHORS

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

DEFINITION

RESULT 5 AF308698 LOCUS

1201 ACCAGTTTCCCCTGTA 1261 TGCCTCCTCAAGTACC 1261 TGCCTCCTCAAGTACC 1321 TGCAATCCTGAGGAAT 1321 TGCAATCCTGAGGAAT	1381 CAGGAGTACAGGAGGA 1381 CAGGAGTACAGGAGGA 1441 CCAGAAATCATCTTCC	1501 GCCACACTIGICACA 	1561 TTTGGGAACTGTGC 1561 TTTGGGACTGTGTC 1621 GCTGTGTTTGTGTCC 	1681 CAGAGAGAACGCGCCT 	1741 CCCAACCAGCTCAAAC 	1801 CACATCAGIAIGAITC 1801 CACATCAGIAIGAITC	1861	1921	1981	2041	2101	2161	2221	2281 CCCAAGCTGATTCCCC
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	AACGGTGCTCGCCTGGACAACATCTGACAATTCAACAATTA AAGGTTGCTCGCCTGGACAACATATTCCTGACACGAACGTGATCTTGGGGGC		ATAGAACTGGGTGTGGGGCCCCACTCTGCCCCAGAATACGAGGATGAAACCATGACAGTT			GTAGCTTTCATCTGTAAGCTTCACTTAAAGAGGAAACTTCTTGGTGCTCAAAGCAAAG 	. GAGATGGGCCTCCCAGTTGGGACAGCTGCCATCGCTCCCATCATTGCTGCTGTCAAGGAC	GGGAAAGCATCACTCATGAAGGAAGAGATTTTGGCTGAAGAGCTGTGTACTCCTCCA 	. GATCCTGGTGCTGTTTGTGGTGGTAGAATGTCCAGATGAAAGCTTCATTCA	TGTGAGAATGCCACCTTTCAGAGGTACCAAGGAAAGGCAGATGCCCCGTGGCCTTGGTG	GTTCACATGGCCCCAGCATCTGTGCTTGTGGACAGCAGGTACCAGCAGTGGATGGA	TTTGGGCCTGACACCCAGCACTTGGTCCTGAATGAGAACTGTGCCTCAGTTCACAACTTTTTGGGCCTCAGTTCACAACTTTTTTGGGCCTGACACTCAGTTCACAACTTTTTTGGGCCTCAGTTCACAACTTTTTTTT	CGCAGCCACAAGATTCAAACCCAGCTCAACCTCATCCACCGGACATCTTCCCCCTGCTC	- accagiticcgcigtaagaagaggccccacccicagigigigigigigigigiaa
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Isogai, T. and Otsuki, T.

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Submitted (16-FEB-2000) Takao Isogai, Helix Research Institute,
Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan

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NEDO human cDNA sequencing project supported by Ministry of
International Trade and Industry of Japan; CDNA full insert
sequencing: Research Association for Biotechnology; CDNA library
construction, 5' & 3'-end one pass sequencing and clone selection:
Helix Research Institute (supported by Japan Key Technology Center
etc.) and Department of Virology, Institute of Medical Science,
University of Tokyo.
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/Drotein 104=18AA91666.1"

/db xref="G1:7022622"

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APVALVVHMAPASVLUDSRYQQWMERRGPDTGHLVLKRGNFLKQPYGCKQL
APDIFPLLTSFRCKEGPTLSVPMVQGECLLKYQLRPRREWQRDAIITCNPEEFIVEAL
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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/note="cloning vector: pME18SFL3-mRNA from NT2 neuronal
precursor cells after 2-weeks retinoic acid (RA)
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                                                                                                                                                    2401 GGCGGCCTGGAGGATGGGGAGCCTCAGCAGAAACGGGCCCACACAGAGGAGCCACAGGCC
                                                                                                                       GGCGGCCTGGAGGATGGGGAGCCTCAGCAGAAGCGGGCCCCACACAGAGGAGCCACAGAGG
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oligo capping; fis (full insert sequence).
Homo sapiens teratocarcinoma cell line:NT2
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/organism="Homo sapiens"
/db xref="taxon:9606"
/clone="NT2RP2000985"
/cell line="NT2"
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Homo Sapiens
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TSLLLDGGGTFGQLCRHYGDQVDRVLGTLAAVEVSHLHABHTGLSBILLQRERALA
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SSLLRTCDLEEFQTCLVRHCKHAFGCALVHTSGWTVVYSGDTMPCEALVRMGKDATLL
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KVGVAPDHWKVCLOGPFTMPKLIPPLKALFAGDIEBWEBRREKRELRQVRAALLSREL
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APVALVVHMAPESVLVDSRYQWMERFGPDTQHLVLABNCAAVHNLRSHKIGTQLNLI
HUED IFPLITZPFCKKEGPPTLSVPMVQSECLLKYQDRPREMORDAIITCNPEEFIVEA
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LISALRTCLEDGLEFGTCLVRYKGHAFGGALVHTSMIPAGNTACELLYRMCKDATL
LIHEATLEDGLEEFAVEKTHSTTSQAISVGRRNNAEFIMLNHFSQRYAKVPLFSPNFN
EKVGVAPDHMKVCFGDFFTMPKLIPPLKALFAGDIEEMEERREKRELRQVRAALLSGE
LAGGLEDGEPQQKRANTQR
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Javigana, S.V., Simard, J., Teng, D.H.F., Baumgard, M., Beck, A.,
Camp, N.J., Carillo, A.R., Chen, Y., Dayanath, P., Desrochers, M.,
Dumont, M., Farnham, J.M., Frank, D., Frye, C., Ghaffari, S.,
Gupte, J.S., Hu, R., Iliev, D., Janecki, T., Kort, E.N., Laity, K.E.,
Leavitt, A., Leblanc, G., McArthur-Morrison, J., Pederson, A., Penn, B.,
Peterson, K.T., Reid, J.B., Richards, S., Schroeder, M., Smith, R.,
Woodland, A.-M., Labrie, F., Swensen, J., Thomas, A., Tranchant, M.,
and Cannon-Albright, L.A.
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/organism="Gorilla gorilla"
/db_xref="taxon:9593"
1. .2893
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Submitted (27-SEP-2000) Myriad
Lake City, UT 84103, USA
Location/Qualifiers
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Sisogai, T. and Yamamoto, J.

Direct Submission

L. Submitted (04-JUL-2002) Takao Isogai, FLJ Project (HRI Team); 2-6-7

Bisogai, T. and Yamamoto, J.

Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan

(E-mall:genomicsehri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)

MEDO human CDNA sequencing project supported by Ministry of Bronomy, Trade and Industry of Japan, CDNA full insert sequencing:

Research Association for Bistechnology (RAB); cDNA library construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: HRI and RAB; annotation; HRI and RAB. ï AK094687

Homo sapiens cDNA FLJ37368 fis, clone BRAMY2024530, highly similar to Homo sapiens prostate cancer susceptibility protein HPC2/ELAC2 Tashiro, H., Yamazaki, M., Watanabe, K., Kumagai, A., Itakura, S., Fukuzumi, Y., Fujimori, Y., Komiyama, M., Sugiyama, T., Irie, R., Otsuki, T., Sato, H., Wakamatsu, A., Ishii, S., Yamanoto, J., Isono, Y., Kawai-Hio, Y., Saito, K., Nishikawa, T., Kimura, K., Yamashita, H., Matsuo, K., Nakamura, Y., Sekine, M., Kikuchi, H., Kanda, K., Wangatsuma, M., Murakawa, K., Kanehori, K., Takahashi-Fujii, A., Oshima, A., Sugiyama, A., Kawakami, B., Suzuki, Y., Sugano, S., Nagahari, K., Masuho, Y., Nagai, K., and Isogai, T., Nagai, K., and Isogai, T., Nagai, K., Mann, CDNA sequencing project Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 238 ATGTGGGGGCTTTTGCTCGCTGCTGCGGTCCGGGCCGGACGCACCACCATGTCGCAGGCACGC 118 61 ACCATATOGOAGGOACCGGCGGCGGGGGGGCGGCGAAGGACCCGCTGCGGCACCTG 120 ----GGCGTTCAGAGACTCATGCAGGAGCACAAGTTA 301 9 cecaceceagagaagcecegaccercegegrecrecegegececeaaacaccerere CGCACGCGAGAGAGCGCGGACCGTCGGGGTGCTCCGGCGGCCCCAAACACCCGTGTACCTG CAGGTGGTGGCAGCGGGTAGCCGGGACTCGGGCGCCGCGCTCTACGTCTTCTCCGAGTTC AACCGGTATCTCTTCAACTGTGGAGAGGCGTTCAGAGACTCATGCAGGAGCACAAGTTA 1 ATGTGGGCGCTTTGCTCGCTGCTGCGGGTCCGCGGCCGGACGCACCATGTCGCAGGGACGC Length 2907; oligo capping; fis (full insert sequence). Homo sapiens amygdala cDNA to mRNA, clone_lib:BRAMY2 clone:BRAMY2024530. Indels /tissue type="amygdala" /clone lib="BRAMY2" /note="cloning vector: pME18SFL3" 788 c 839 g 584 t 5; DB 9; 94.7%; Score 2349; I 97.5%; Pred. No. 0; Live 0; Mismatches CAGGTGGTGGCAGCGGGTAGCCGGGACTCG-----/organism="Homo sapiens" /db_xref="taxon:9606" /clone="BRAMY2024530" Location/Qualifiers AK094687.1 GI:21753794 (bases 1 to 2907) Conservative Homo sapiens Unpublished Best Local Similarity Matches 2419; Conserv AK094687 Query Match BASE COUNT ORIGIN AK094687 LOCUS DEFINITION ORGANISM REFERENCE AUTHORS TITLE JOURNAL REFERENCE AUTHORS TITLE JOURNAL 59 119 121 179 181 239 241 269 ACCESSION VERSION KEYWORDS SOURCE FEATURES COMMENT 엄 us-09-434-382-1.rge

S a	301	AAGGTTGCTCGCCTGGACAACATATTCCTGACACGAATGCACTGGTCTAATGTTGGGGGC 360
Qy Dp	361	TTAAGTGGAATGATTCTTAATAAGGAAACCGGGCTTCCAAAGTGTGTATCTTCTGGA 420
& g	421	48
9 G	481	ACTGGCTGTGCGGCCCCCTCTGCCCCGGAATACGAGGATGAAACCATGACAGTT 5
95 G	541	TACCAGATCCCCATACACAGGAAACACAGAGAAAGCACCAACCA
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                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (04-JUL-2002) Takao Isogai, FLJ Project (HRI Team); 2-6-7 Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan (E-mall:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986) MEDO human CDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; CDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA full insert sequencing: Construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5- & 3'-end one pass sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: HRI and RAB; annotation: HRI and RAB.
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clone:BRACE2010203.
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                                                                                                                                                                             762 CTTGGTGCTCAAAGCAAAGGAGATGGGCCTCCCCAGTTGGGACAGCTGCCATCG
/note="cloning vector: pME18SFL3"
582 c 613 g 438 t
                                                                                    Score 1715.2;
Pred. No. 0;
0; Mismatches
                                                                                         69.1%;
99.8%;
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Matches 1717;
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Direct Submission
Submitted (14 FEB-2002) Sumio Sugano, Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure, Human Genome Center; Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan (E-mail:cdnal@ims.u-tokyo.ac.jp, Tel:81-3-5449-5286,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology; cDNA library construction, 5. & 3'-ed one pass sequencing: Departent of Virology and Human Genome Center, Institute of Medical Science, University of Tokyo (partly supported by Science and Technology Agency).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AK074244. GI:18676795
AK074244.1 GI:18676795
Oligo capping; fis (full insert sequence).
Homo sapiens hepatoma cell_line:HepG2 cDNA to mRNA, clone_lib:HEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kawabata, A., Hikiji, T., Kobatake, N., Inagaki, H., Ikema, Y., Okamoto, S., Okitani, R., Ota, T., Suzuki, Y., Obayashi, M., Nishi, T., Shibahara, T., Tanaka, T., Nakamura, Y., Isogai, T. and Sugano, S. NEDO human cDNA sequencing project Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            clone:HEP03495.
Homo sapiens
Eukaryots, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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  2357 AGCTGCGGCAGGTGCGGGCGCCCTCTGTCCAGGGAGCTGGCAGGCGGCCTGGAGGATG
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                                                                        CCCAAGCCATCAGCGTGGGGATGCGGATGAACGCGGAGTTCATTATGCTGAACCCTTCA
                                                                                                                                                                 GCCAGCGCTATGCCCAGCCCCCTCTTCAGCCCCCAACTTCAGCGAGAAAGTGGGAGTTG
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                                                                                                                                       GCCAGCGCTATGCCAAGGTCCCCCTCTTCAGCCCCCAACTTCAGCGAGAAAGTGGGGAGTTG
                                                                                                                                                                                                                                 CCTTTGACCACATGAAGGTCTGCTTTGGAGACTTTCCAACAATGCCCAAGCTGATTCCCC
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ACCESSION VERSION KEYWORDS SOURCE

ORGANISM

REFERENCE AUTHORS TITLE JOURNAL

COMMENT

AUTHORS

REFERENCE

TITLE JOURNAL

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1722 CCCTTTGCTGGTGGTTGCCCCCAACCAGCTCAAAGCCTGGCTCCAGCAGTACCACAACCA 1781

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Submitted (27-SEP-2000) Myriad Genetics, Inc., 320 Wakara Way, Salt
Lake City, UT 84103, USA
4 (bases 1 to 2712)
Tavtigian, S.V., Simard, J., Teng, D.H.F., Baumgard, M., Beck, A.,
Camp, N.J., Carillo, A.R., Chen, Y., Dayananth, P., Desrochers, M.,
Dumont, M., Farnham, J.M., Frank, D., Frye, C., Ghaffari, S.,
Dumont, M., Leblanc, G., McArthur-Morrison, J., Pederson, A., Penn, B.,
Peterson, K.T., Raid, J.E., Richards, S., Schroeder, M., Smith, R.,
Snidt, A., Labrie, F., Swensen, J., Thomas, A., Tranchant, M.,
and Cannon-Albright, L.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (26-DEC-2000) Myriad Genetics, Inc., 320 Wakara Way, Salt Lake City, UT 84103, USA Sequence update by submitter.

On Dec 26, 2000 this sequence version replaced gi:10946492.

Location/Qualifiers
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IAFDHMKVCFGDFPTVPKLIPPLKALFAGDIEEMVERREKRELRLVRAALLTQQADSP
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Tavigan, S.V., Simard, J., Teng, D.H.F., Baumgard, M., Beck, A., Camp, N.J., Carillo, A.R., Chen, Y., Dayananth, P., Desrochers, M., Dumont, M., Farnham, J.M., Frank, D., Frye, C., Ghaffari, S., Gupte, J.S., Hu, R., Iliev, D., Janeck, T., Kort, E.N., Lairy, K.E., Peravitt, A., Leblanc, G., McArthur-Morrison, J., Pederson, A., Penn, B. Peterson, K.T., Reid, J.E., Richards, S., Schroeder, M., Smith, R., Snyder, S.C., Swedlund, B., Swensen, J., Thomas, A., Tranchant, M., Moodland, A.-M., Labrie, F., Skolnick, M.H., Neuhausen, S., Rommens, J., Mouse ortholog f human HPC2/ELAC2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tavtigian, S.V., Simard, J., Teng, D.H.F., Baumgard, M., Beck, A.,
Tavtigian, S.V., Simard, J., Teng, D.H.F., Baumgard, M., Beck, A.,
Tavtigian, S.V., Simard, J., Teng, D.H.F., Bayanarth, P., Desrochers, M.,
Dumont, M., Farnham, J.M., Frank, D., Frye, C., Ghaffari, S.,
Gupte, J.S., Hu, R., Illev, D., Janecki, T., Kort, E.N., Laity, K.E.,
Leavitt, A., Leblanc, G., McArthur-Morrison, J., Pederson, A., Penn, B.
Peterson, K.T., Reid, J.E., Richards, S., Schroeder, M., Smith, R.,
Woodland, A.-M., Labrie, F., Skonick, M.H., Neuhausen, S., Rommens, J.
   candidate prostate cancer susceptibility gene at chromosome 17p t. Genet. 27 (2), 172-180 (2001)
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/product="ELAC2"
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Tavtigian, S.V., Simard, J., Teng, D.H.F., Abtin, V., Baumgard, M., Beck, A., Camp, N.J., Carillo, A.R., Chen, Y., Dayananth, P., Desrochers, M., Dumont, M., Farnham, J.M., Frank, D., Frye, C., Ghetrari, S., Gupte, J.S., Hu, R., Illev, D., Janecki, T., Kort, E.N., Laity, K.E., Leavitt, A., Leblanc, G., MoArthur-Morrison, J., Schroeder, M., Smith, R., Snyder, S.C., Swednen, J., Thomas, A., Tranchant, M., Woodland, A.M., Labrie, F., Skolnick, M.H., Neuhausen, S., Rommens, J. and Cannon-Albright, L.A.
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Query Match 68.0%; Score 1686.2; DB 10; Length 2712; Best Local Similarity 82.2%; Pred. No. 0; Matches 1982; Conservative 0; Mismatches 408; Indels 21; Gaps	SCCGCCGCGAGCGCCGCGCAAGGACCC	54 GGCACCATGTCGCAGGGTTCGGCTCGGCCGGCCGTCCAAAGACCCACTGCGACAC	DD 114 CTGCGTACGGGGGGGGGCCCCGGGTCCCGGGGGCCCCGAACGCCGTAC 167 DD 114 CTGCGTACGCGGGAGAAGCGCGGCCCGGGTCCCGGGGGGCCCCGAACACCGTGTAC 167	Qy 178 CTGCAGGTGGCAGCGGGTAGCCGGGACTCGGGCGCGCGCG	Db 168 CTGCAGGTGGTGGGGGGGGGGGGGGGGGGGGGGGGGGGG	OY 238 TTCAACCGGTATCTCTTCAACTGTGGAGAGGCGTTCAGAGACTCATGCAGGAGCACAGG 297 Db 228 TACAACAGGTACCTTTTTAACTGCGGAGAAGGCGTCCAACGACTTATGCAGGAACACAAA 287	298 TTAAAGGTTGCTCGCCTGGACAACATATTCCTGACGGAATGCACTGGTCTAATGTTGGG	Db 288 CTGAAAGTCGCTCGCTTGGACAACATCTTTCTGACTCGGATGCATTGGTCAAATGTTGGG 347	Oy 358 GGCTTAAGTGGAATGATTCTTACTTTAAAGGAAACCGGGCTTCCAAAGTGTGTACTTTCT 417		478 GGAATAGAACTIGGCTGTGCGCCCCACTCTGCCCCAGAATACGAGATGAAACCATGACA	Db 468 GGAATAGAACTGGCCGTGCGGCCTCACTCTGCACCAGAATACAAGGATGAGACCATGACT 527	OY 538 GTTTACCAGATCCCCATACACAGTGAACAGGGGGAAAGCAACCAAC	CCAGAAAGGCTCTCAGCAGGTCAGTCCAGAGGGATCTTCAGACTCCGAGTCGAATGAA	Db 588 CCCAGAACATCTCCCAACAGCTCACCCAAACAGTCATCGGACTCTGGATCAGCTGAA 647	QY 658 AATGACCACCTCCACA	706 GACTCTTCCCTGGTCGTAGCTTTCATCTGTAAGCTTCACTTAAAGAGAAGAACTTCTTG	DD 708 GACCCCTCCTTAGTGGTAGCTTTTGTCTGCAAGCTTCACTTGAGGAAAGGAAACTTCTTG 767 Ov 766 GTGCTCAAAGCAAAGGAAAGGCCTCCCAGTTGGGACACTGCCATGGCTCCCATCATT 825	768 GIGCTTAAAGGAAGCIGGCCTTCCTGTTGGGACGGCCGCCATTGCACCATCATT	OY 826 GCTGCTGTCAAGGACGGAAAAGCATCACTCATGAAGGAAG	828 GCTGCTGTCAAGGACGGGAAGAGTATCACTTACGAAGGAAG	OY 886 CTGTGTACTCCTCCAGATCCTGGTGGTGGTGGTGGTAGAATGTCCAGATGAAAGC 945	946 TICATICAACCCATCTGTGAGAATGCCACCTTTCAGAGGTACCAAGGAAAGGCAGATGCC	Db 948 TTCATCCTGCCCATCTGTGAGAACGACACCTTTAAAAGGTACCAGGCAGAGGTGATGCA 1007 Ov 1008 CCCGTGGCCGTAGGTAGAAAAAAAAAAAAAAAAAAAAAA	1008 CCTGTGGCGCTGGTGCACATAGCCCCAGAATCTGTACTCACAGCAGAGATACCAG 106	Oy · 1066 CAGTGGATGGAGGGTTTGGGCCTGACACCCAGCACTTGGTCCTGAATGAGAACTGTGCC 1125

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (04-JUL-2002) Takao Isogai, FLJ Project (HRI Team); 2-6-7 Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986) NBDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5. & 3.-end one pass sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: HRI and RAB; annotation: HRI and RAB.

Location/Qualifiers

rce | 1. 2793 | 1. 22793 | 1. 22793 | 1. 22793 | 1. 22793 | 1. 22793 | 1. 22793 | 1. 22793 | 1. 22793 | 1. 22793 | 1. 22793 | 1. 22793 | 1. 22793 | 1. 22793 | 1. 22793 | 1. 22793 | 1. 22793 | 1. 22793 | 1. 22793 | 1. 22793 | 1. 22793 | 1. 22793 | 1. 22793 | 1. 22793 | 1. 22793 | 1. 22793 | 1. 22793 | 1. 22793 | 1. 22793 | 1. 22793 | 1. 22793 | 1. 22793 | 1. 22793 | 1. 22793 | 1. 22793 | 1. 22793 | 1. 22793 | 1. 22793 | 1. 22793 | 1. 22793 | 1. 22793 | 1. 22793 | 1. 22793 | 1. 22793 | 1. 22793 | 1. 22793 | 1. 22793 | 1. 22793 | 1. 22793 | 1. 22793 | 1. 22793 | 1. 22793 | 1. 22793 | 1. 22793 | 1. 22793 | 1. 22793 | 1. 22793 | 1. 22793 | 1. 22793 | 1. 22793 | 1. 22793 | 1. 22793 | 1. 22793 | 1. 22793 | 1. 22793 | 1. 22793 | 1. 22793 | 1. 22793 | 1. 22793 | 1. 22793 | 1. 22793 | 1. 22793 | 1. 22793 | 1. 22793 | 1. 22793 | 1. 22793 | 1. 22793 | 1. 22793 | 1. 22793 | 1. 22793 | 1. 22793 | 1. 22793 | 1. 22793 | 1. 22793 | 1. 22793 | 1. 22793 | 1. 22793 | 1. 22793 | 1. 22793 | 1. 22793 | 1. 22793 | 1. 22793 | 1. 22793 | 1. 22793 | 1. 22793 | 1. 22793 | 1. 22793 | 1. 22793 | 1. 22793 | 1. 22793 | 1. 22793 | 1. 22793 | 1. 22793 | 1. 22793 | 1. 22793 | 1. 22793 | 1. 22793 | 1. 22793 | 1. 22793 | 1. 22793 | 1. 22793 | 1. 22793 | 1. 22793 | 1. 22793 | 1. 22793 | 1. 22793 | 1. 22793 | 1. 22793 | 1. 22793 | 1. 22793 | 1. 22793 | 1. 22793 | 1. 22793 | 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AKU94012 2793 bp mRNA linear PRI 15-JUL-2002 Homo sapiens cDNA FLJ36693 fis, clone UTERU2008901, highly similar to Homo sapiens putative prostate cancer susceptibility protein HPC2/ELAC2 mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tashiro, H., Yamazaki, M., Watanabe, K., Kumagai, A., Itakura, S., Fukuzumi, Y., Fujimori, Y., Komiyama, M., Sugiyama, T., Irie, R., Otsuki, T., Sato, H., Wakamatsu, A., Ishii, S., Yamamoto, J., Isono, Y., Kawai-Hio, Y., Saito, K., Nishikawa, T., Kimura, K., Yamashita, H., Matsuo, K., Nakamura, Y., Sekine, M., Kikuchi, H., Kanda, K., Wagatsuma, M., Murakawa, K., Kanehori, K., Takahashi-Fujii, A., Oshima, A., Sugiyama, A., Kawakami, B., Suzuki, Y., Sugano, S., Nagahari, K., Masuho, Y., Nagai, K., and Isogai, T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                               GACTTCCCGACAGTGCCCAAAGTGCTGATTCCCCCACTGAAGGCCCTGTTTGCAGGTGACATT
                                                                                                                                                                                                                                                            AATGCGGGGTTCATCATGCTGAACCACTTCAGTCAGCGGTACGCCAAGATCCCCCTTTTTC
                                                                            GACTITCCAACAATGCCCAAGCTGATTCCCCCACTGAAAGCCCTGTTTGCTGGCGACATC
                                                                                                                                                                                                                             GAGGAGATGGAGGAGCGCAGGGAGAAAGCGGGAGCTGCGGCAGGTGCGGGGCGCCCTCCTG
                                                                                                                                                                                                                                                                                                                       2386 TCCAGGGAGCTGGCAGGCGGCCTGGAGGATGGGGAGCCTCAGCAGAAGCGGGCCCACACA
                                             AGCCCCAACTTCAGCGAGAAAGTGGGAGTTGCCTTTGACCACATGAAGGTCTGCTTTGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 insert sequence).
to mRNA, clone_lib:UTERU2
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/db_xref="taxon:9606"
/clone="UTERU2008901"
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/clone Tib="UTERU2"
/note="cloning vector:
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Isogai, T. and Yamamoto, J.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AK094012.1 GI:21752986 oligo capping; fis (full Homo sapiens uterus cDNA clone:UTERU2008901.
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AC005277 118788 bp DNA linear PRI 23-JUL-1998
Homo sapiens chromosome 17, clone hRPK.597_M_12, complete sequence.
AC005277
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                     1606 TCACCCTTGCTGGTGGTTGCCCCCCAACCAGCTCAAAGCCTGGCTCCAGCAGCACAAA
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                  Score 823; DB 9; Le
Pred. No. 7.1e-181;
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                                                                               Conservative
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family="AluJo"
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/rpt_family="LIME3A"
complement (20821. .21069)
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[ement (1100)
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20263. , 205en
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/rpt_family="LTR16C"
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/rpt family="LTR16C"
12453. 12725
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complement(19638. .19896)
/rpt_family="MIR"
complement(19971. .20260)
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/rpt_family="MER5A"
6830. .7013
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                                 /rpt_family="(TAAA)n"
complement(4328. .4608)
/rpt_family="AluSx"
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/rpt_family="Alusp"
5219...5479
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/rpt_family="AluSp"
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9662. .9829
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7319. .7581
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/rpt_family="AluJb"
8039. .8333
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1014. .7318
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431. .9460
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                                                                                                                                                                                                                                                family="MER34"
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4118. .14143
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.8271. .18311
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complement(11302.
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                                                                                                                                                                                  .5479
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                                                  CE 2 (bases 1 to 118788)

Birren, B., Fasman, K., Linton, L., Nusbaum, C., Lander, E., Allen, N., Baker, J., Baldwin, J., Barna, N., Beckerly, R., Benn, J., Boatin, C., Baker, J., Baldwin, J., Castle, A., Cerny, J., Cooke, P., Depayre, E., Boutwell, C., Brown, A., Castle, A., Cerny, J., Cooke, P., Depayre, E., Devon, K., Donelan, L., Etemadi, S., Ferreira, P., Fitzhugh, W., Forrest, C., Funke, R., Gage, D., Gardyna, S., Gensheimer, S., Geraigery, K., Gilmartin, T., Grant, G., Hagos, B., Harris, K., Marquis, N., Mozewan, P., McGurk, A., McKernan, K., Maddrim, J., Molla, M., Morris, W., Morrow, J., Mychaleckyj, J., Nachman, A., Nahf, R., Naylor, J., Niloff, M., O'Connor, T., Pavlin, B., Peterson, K., Riley, R., Roberts, D., Rossello, R., Stone, C., Strickland, C., Subramanian, A., Torruella-Miller, I., Vassiliev, H., Vo, A., Wagner, A., Wang, B., Wheeler, J., Wu, Y., Ye, W.J., Zhao, J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Summission

Submitted (10-UTL-1998) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

1 (Dases 1 to 11878)

Birten, B., Fasman, K., Linton, L., Nusbaum, C., Lander, E., Allen, N., Baker, J., Baldwin, J., Barna, N., Beckerly, R., Benn, J., Boatin, C., Boute, C., Brown, A., Castle, A., Cerry, J., Cooke, P., Depayre, E., Devon, K., Dewar, K., Donelan, L., Etemadi, S., Ferreira, P., FitzHugh, W., Forrest, C., Funke, R., Gardyna, S., Gensheimer, S., Geraglery, K., Gilmartin, T., Grant, G., Hagos, B., Harris, K., Horton, L., Howland, J.C., Hui, L., Jacotot, L., Kann, L., Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., Meltin, J., Molla, M., Morris, W., Morrow, J., Mychaleckyj, J., Nahf, R., Naylor, J., Nioff, M., O'Connor, T., Pavlin, B., Peterson, A., Nahf, R., Naylor, J., Nioff, M., O'Connor, T., Pavlin, B., Stange-Thomann, N., Stilwell, J., Stojanovic, N., Stone, C., Strickland, C., Subramanian, A., Torruella-Miller, I., Vassiliev, H., Vo, A., Mang, B., Wheeler, J., Wu, Y., Ye, W.J., Zhao, J. and J. Cody, M., Magner, A., Wang, B., Wheeler, J., Wu, Y., Ye, W.J., Zhao, J. and J. Cody, M., Wagner, A., Wang, B., Wheeler, J., Wu, Y., Ye, W.J., Zhao, J. and J. Cody, M., Wagner, A., Wang, B., Wheeler, J., Wu, Y., Ye, W.J., Zhao, J. and J. Cody, M., Wagner, A., Wang, B., Wheeler, J., Wu, Y., Ye, W.J., Zhao, J. and J. Cody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (23-JUL-1998) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Ull 23, 1998 this sequence version replaced gi:3335015. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Only the first 118.8 kilobases of this clone are being submitted.
The remainder overlaps accession number AC005274 (WICGR project
Birren,B., Fasman,K., Linton,L., Nusbaum,C. and Lander,E.
Homo sapiens chromosome 17, clone hRPK.597_M_12
Unpublished
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http://ftp.genome.washington.edu/RM/RepeatMasker.html
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clone lb="RPCI-11 human BAC library"
755. 884
rpt_family="MIR"
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db_xref="taxon:9606"
chromosome="17"
map="17"
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/rpt_family="L2"
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Bukaryota, Metazoa, Chordata, Catarrhini, Hominidae, Homo.

B. 1 (bases 1 to 740)
S. Tattigian, S. V., Simard, J., Teng, D. H.F., Baumgard, M., Beck, A., Cartigian, S. V., Simard, J., Teng, D. H.F., Baumgard, M., Beck, A., Camp, N. J., Carillo, A. R., Chen, Y., Dayananth, P., Desrochers, M., Dumont, M., Farnham, J. M., Frank, D., Frye, C., Ghaffari, S., Gupte, J. S., H., R., Illev, D., Janecki, T., Kort, E. N., Laity, K.E., Leavitt, A., Leblanc, G., McArthur-Morrison, J., Pederson, A., Penn, B., Peterson, K. T., Reid, J. E., Richards, S., Schroeder, M., Smith, R., Snyder, S. C., Swedlund, B., Swensen, J., Thomas, A., Tranchant, M., Woodland, A.-M., Labrie, F., Skolnick, M.H., Neuhausen, S., Rommens, J. and Cannon-Albright, L.A.
A strong candidate prostate cancer susceptibility gene at
                                                                                                                   Homo sapiens
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae, Homo.

Mammalia; Eutheria; Primates; Catarrhini; Hominidae, Homo.

1 (bases 1 to 679)

Kutsenko,A.S., Gizatullin,R.Z., Al-Amin,A.N., Wang,F., Kvasha,S.M., Podowski,R.M., Matushkin,Y.G., Gyanchandani,A., Muravenko,O.V.,

Levitsky,V.G., Kolchanov,N.A., Protopopov,A.I., Kashuba,V.I.,

Kisselev,L.L., Wasserman,W., Wahlestedt,C. and Zabarovsky,E.R.

Not! flanking sequences: a tool for gene discovery and verification of the human genome

Of the human genome
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Submitted (16-MAY-2001) Microbiology and Tumorbiology Centre,
Karolinska Institute, Theorells vag, 3, Box 280, Stockholm 171 77,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 GTGCTCCGGGGCCCAAACACCGTGTACCTGCAGGTGGTGGCAGCGGGTAGCCGGGACTC 120
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Homo sapiens putative prostate cancer susceptibility protein HPC2/ELAC2 gene, exon 17 and partial cds.
Homo sapiens genomic sequence surrounding NotI site, clone NL6-B020C.
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Pred. No. 1.1e-25;
0; Mismatches 7;
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/db_xref="taxon:9606"
/clone="NL6-B020C"
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95.8%;
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Zabarovsky, E.R.
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Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CGCACGCGAGAGAGCGCGGACCGTCGGGGGTGCTCCGGCGGCCCCAAACACCGTGTACCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 78682 CGCACGCGAGAGAAGCGCGGGACCGTCGGGGGTGCTCCGGCGCCCCAAACACCCGTGTACCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CAGGTGGTGGCAGCGGGTAGCCGGGACTCGGGCGCCCGCGCTCTACGTCTTCTCCGAGTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 118788;
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                                                                                                                                                                                                                                                                                                                                                                        note="Single-stranded coverage."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 10.0%; Score 247.4; DB 9
Best Local Similarity 97.7%; Pred. No. 1.1e-46;
Matches 251; Conservative 0; Mismatches 6
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          /rpc_family="(TAAA)"
complement(21101. .21338)
/rpc_family="Alusx"
complement(21348. .21598)
/rpc_family="L144" .21598)
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complement(26576. .26781)
/rpt family="MERGB"
complement(26912. .26990)
/rpt family="MER21B"
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24852. .25199 /rpt_family="L2"
complement(25697. .25985)
/rpt_family="MLTID"
25816. .25895
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /rpt_family="MER21B"
18034. .28197
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complement (26122. .26291)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'rpt_family="(CAAAA)n"
86456, .26480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /rpt_family="AluSx"
complement(27291. .2
                                                                                                                                                                                                                                                                                                                                                                                                                                                   rpt family="MLT1D"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28843. .28916
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28920. .29005
                                                                                                                                                                                                                                               family="AluSq"
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                                                                                                                                                                rpt_family="AluJo"
2151. .22562
rpt_family="MSTA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            family="LTR28"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /rpt_family="MIR"
29140. .29233
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                                                                                                                                                                                                                     3978. .24287
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28843.
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Camp,N.J., Carillo,A.R., Chen,Y., Dayananth,P., Desrochers,M.,
Camp,N.J., Carillo,A.R., Chen,Y., Dayananth,P., Desrochers,M.,
Dumont,M., Farnham,J.M., Frank,D., Frye,C., Ghaffari,S.,
Gupte,J.S., Hu,R., Illav,D., Janecki,T., Kort,B.N., Labtry,K.E.,
Leavitt,A., Leblanc,G. McArthur-Morrison,J., Pederson,A., Penn,B.,
Peterson,K.T., Reid,J.E., Richards,S., Schroeder,M., Smith,R.,
Snyder,S.C., Swedlund,B., Swensen,J., Thomas,A., Tranchant,M.,
Woodland,A.-M., Labrie,F., Skolnick,M.H., Neuhausen,S., Rommens,J.
and Cannon-Albright,L.A.
Direct Submission
L. Submitted (12-SEP-2000) Myriad Genetics, Inc., 320 Wakara Way, Salt
Lake City, UT 84108, USA
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HPC2/ELAC2"
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326 TGTGGTGAGGGCACATTTGGGCAGCTGTGCCGTCATTACGAGACCAGGTGGACAGGGTC 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1486 ATTCGAAATGTCAGTGCCACACTTGTCAACATAAGCCCCGACACGTCTCTGCTACTGGAC 1545
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 5.9%; Score 146.2; DB 9; Length 740; Best Local Similarity 89.7%; Pred. No. 3.3e-23; Matches 157; Conservative 0; Mismatches 18; Indels 0
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                                                                                                                                                                                                                                                                                                                                                               1. 740
/organism="Homo sapiens"
/db_xref="taxon:9606"
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Sequence 3, Appli
Sequence 223, App
Sequence 225, App
Sequence 221, App
Sequence 210, App
                                                                                                               May 17, 2003, 15:56:54 ; Search time 139.603 Seconds (without alignments) 5450.193 Million cell updates/sec
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GenCore version 5.1.5
Copyright (c) 1993 - 2003 Compugen Ltd
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US-09-564-805-3

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US-09-564-805-221

US-09-564-805-21

US-09-564-805-28

US-09-564-805-18

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US-09-564-805-6
US-09-564-805-9
                                                                                                                                                                                                                                                                                                                                           441362 segs, 153338381 residues
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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seq length: 200000000
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Oy G	361 TTAAGTGGAATGATTCTTACTTTAAAGGAAACCGGGCTTCCAAAGTGTGTACTTTCTGGA 420 	
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\(\delta \)	541 TACCAGATCCCATACACAGAGAGGAGGAAAGCACCAACCA	
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qa	721 GTAGCTTTCATCTGTAAGCTTCACTTAAAGAGGAAACTTCTTGGTGCTCAAAGCAAAG 780 	
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oy du	841 GGGAAAGCATCACTCATGAAGGAAGAGATTTTGGCTGAAGACTGTGTACTCCTCCA 900 	
5. 6. 6. 6.	901 GATCCTGGTGCTGCTTTTGTGGTGGTAGAATGTCCAGATGAAAGCTTCATTCA	
6 6 6	961 TGTGAGAATGCCACCTTTCAGAGGTACCAAGGAAAGGCAGATGCCCCCGTGGCCTTGGTG 1020 	
Oy 1(021 GTTCACATGGCCCCAGCATCTGTGCTTGTGGACAGCAGGTACCAGCAGTGGATGGA	
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APPLICANT: Tavigian, Sean V.
APPLICANT: Tavigian, Sean V.
APPLICANT: Simard, Joaques
APPLICANT: Simard, Joaques
APPLICANT: Rommens, Joaques
TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility
TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes
TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes
FILE REFERENCE: 2318-258
CURRENT APPLICATION NUMBER: US 60/107,468
PRIOR APPLICATION NUMBER: US 60/107,468
PRIOR APPLICATION NUMBER: 099-11-05
PRIOR FILING DATE: 1998-11-05
PRIOR FILING DATE: 1998-11-05
NUMBER OF SEQ ID NOS: 240
SEQ ID NO 3
SEQ ID NO 3
LENGTH: 2958
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COTHER INFORMATION: coding sequence as in SEQ ID NO:1
US-09-564-805-3
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100.0%; Score 2481;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2481; Conservative 0; Mismatches
                                                                                                  ; Sequence 3, Application US/09564805; Patent No. 6333403; GENERAL INFORMATION:
                                    2461 AAGAAGGTCAGAGCCCAGTGA
                       2461 AAGAAGGTCAGAGCCCAGTGA
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc feature
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US-09-564-805-3
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Sequence 223, Application US/09564805 Patent No. 6333403 GENERAL INFORMATION:

APPLICANT: Tavtigian, Sean V. APPLICANT: Teng, David H.F. APPLICANT: Simard, Jacques

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APPLICANT: Rommens, Johanna M.
APPLICANT: Myriad Genetics, Inc.
TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility
TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes
FILE REPERENCE: 2318-258
CURRENT APPLICATION NUMBER: US/09/564,805
CURRENT APPLICATION NUMBER: US 60/107,468
PRIOR FILING DATE: 1998-11-06
PRIOR FILING DATE: 1998-11-05
PRIOR FILING DATE: 1999-11-05
NUMBER OF SEQ ID NOS: 240
SEQ ID NO 223
LENGTH: 2908
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Pred. No. 0;
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Best Local Similarity 99.4%;
Matches 2465; Conservative
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ORGANISM: Pan troglodytes
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                                                                     Length 2892
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                                                                   Score 2442.6;
Pred. No. 0;
0; Mismatches
                                                                   98.5%;
                                                                                Best Local Similarity 99.0
Matches 2457; Conservative
ORGANISM: Gorilla gorilla
                    ; NAME/KEY: CDS
; LOCATION: (1)..(2478)
US-09-564-805-225
                                                                      Query Match
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qq	1021	
ò	1081	TTTGGGCCTGACACCCAGCACTTGGTCCTGAATGAGAACTGTGCCTCAGTTCACAACCTT 1140
qq	1081	TTTGGGCCTGACACCCCAGCACTTGGTCCTGAATGAGAACTGTGCCTCCAGTTCACAACCTT 1140
δ	1141	CGCAGCCACAAGATICAAACCCAGCTCAACCTCATCCACCCGGACAICTTCCCCCTGCTC 1200
ΩD	1141	CGCAGCCACAAGATTCAAACCCAGCTCAACCTCATCCACCGGACATCTTCCCCCTGCTC 1200
ογ	1201	ACCAGITICGCIGIBAGAGAGGCCCCACCTCAGIGIGCCCATGGITCAGGGIGAA 1260
qq	1201	ACCAGTTTCCCCTGTAAGAAGGAGGCCCCACCCTCAGTGTGCCCATGGTTCAGGGTGAA 1260
ò	1261	TGCCTCCTCAAGTACCAGCTCCGTCCCAGGAGGAGTGGCAGGGAGGCATGCCATTATTACT 1320
QΩ	1261	TGCCTCCTCAAGTACCAGCTCCGTCCCAGGAAGGGAATGGCAGGGATGCCATTATCACT 1320
ογ	1321	TGCAATCCTGAGGAATTCATAGTTGAGGCGCTGCAGCTTCCCGAACTTCCAGCAGAGCCTG 1380
qq	1321	TGCAATCCTGAGGAATTCATAGTTGAGGCGCTGCAGCTTCCCAACTTCCAGGAGTGTG 1380
ò	1381	CAGGAGTACAGGAGGAGTGCGCAGGACGGCCCCAGCAGCAGAAAAAAGAAGTCAGTAC 1440
QQ	1381	CAGGAGTACAGGAGGAGTGCTGCTGCTCCCAGCCCCAGAGAAAAAAAA
δ	1441	CCAGAAATCATCTTCCTTGGAACAGGGTCTGCCATCCCGATGAAGATTCGAAATGTCAGT 1500
qq	1441	CCAGAAATCATCTTCCTTGGAACAGGGTCTGCCATCCCCATGAAGATTCGAAATGTCAGT 1500
ò	1501	GCCACACTIGICAACATAAGCCCCGACACGICTCTGCTACTGGACTGTGGTGAGGGCACA 1560
Ωp	1501	GCCACACTIGLICALITATION OF THE CONTROLL OF THE CONTROLL OF THE CONTROL OF THE CONT
ò		TTTGGGCGGCTGTGCGTCATTACGGAGACCAGGTGGACAGGGTCCTGGGCACCCTGCCT 1620
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٥٨	1621	GCTGTGTTTGTGTCCCACCTGCACGCAGATCACCACACGGCTTGCCAAGTATCTTGCTG 1680
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ò	1681	CAGAGAGAACGCGCCTTGGCATCTTTGGGAAAGCCGCTTCACCCTTTGCTGGTGGTTGCC 1740
DÞ	1681	CAGAGAGAACAAGCCTTGGGCATCTTTGGGAAAGCCCCTTCACCCTTTGCTGGTGGTTGCC 1740
ò	1741	CCCAACCAGCTCAAAGCCTGGCTCCAGCAGTACCACAACCAGTGCCAGGAGGTCCTGCAC 1800
ΩP	1741	CCCAGCCCAGCTCAGCTCGCTCCAGCAGTACCACAACCAGTGCCAGGAGGTCCTGCAC 1800
ò	1801	CACATCAGTATGATTCCTGCCAAATGCCTTCAGGAAGGGGCTGAGATCTCCAGTCCTGCA 1860
Dp	1801	CACATCAGTATGATTCCTGCCAAATGCCTTCAGGAAGGGGCTGAGATCTCCAGTCTGCA 1860
ò	1861	GTGGAAAGATTGATCAGTTCGCTGTTGCGAACAFGTGATTTGGAAGAGTTTCAGACCTGT 1920
QQ	1861	GTGGAAAGATTGATCAGTTCGCTGTTGCGAACATGTGATTTGGAAGAGTTTCAGACCTGT 1920
δy	1921	CTGGTGCGGCACTGCAAGCATTTGGCTGTGCGCTGGTGCACACCTCTGGCTGG
QQ	1921	CTGGTGCGGCACTGCAAGCATGCGTTTGGCTGTGCGCTGGTGCACCTCTGGCTGG
ò	1981	GTGGTCTATTCCGGGGACACCATGCCTGCGAGGCTCTGGTCCGGATGGGGAAAGATGCC 2040
ΩÞ	1981	THITTCGGGGACACCATGCCTGCGAGGCTCTGGTCCGCATGGGGAAAGATGCC

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APPLICANT: Tavigian, Sean V.
APPLICANT: Tavigian, Sean V.
APPLICANT: Tavigian, Sean V.
APPLICANT: Tang, David H.F.
APPLICANT: Romans, Joquans
APPLICANT: Romans, Johanna M.
APPLICANT: Myriad Genetics, Inc.
TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes
FILE REFERENCE: 2318-258
FILE REFERENCE: 2318-258
FILE REFERENCE: 2918-258
FILE REFERENCE: 2918-258
FILE REFERENCE: 1999-11-06
FRIOR APPLICATION NUMBER: US 60/107,468
FRIOR APPLICATION NUMBER: 09/434,382
FRIOR FILING DATE: 1999-11-05
FRIOR FILING DATE: 1999-11-05
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                                                                                                2101 ACACACACAAACGTCCCAAGCCATCAGCGGGGATGCGGATGAGCGGGGGGTTCATT
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Patent No. 6333403
GENERAL INFORMATION:
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; NAME/KEY: CDS
; LOCATION: (1).
US-09-564-805-221
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US-09-564-805-221
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                                                   1279 GACTGCAATACTGATGAATTCATAGCTGAGGCCTTGGAGCTCCCCAGTTTCCAGGAGAGT
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APPLICANT: Tavigian, Sean V.
APPLICANT: Tavigian, Sean V.
APPLICANT: Tavigian, Sean V.
APPLICANT: Tavigian, Sean V.
APPLICANT: Tavigian Seques
APPLICANT: Simmard, Johanna M.
APPLICANT: Myriad Genetics, Inc.
TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility
TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes
FILE REFERENCE: 2318-258
CURRENT APPLICATION NUMBER: US/09/564,805
CURRENT APPLICATION NUMBER: US 60/107,468
PRIOR PILING DATE: 1998-11-06
PRIOR FILING DATE: 1999-11-06
PRIOR FILING DATE: 1999-11-05
NUMBER OF SEQ ID NOS: 240
SOFTWARE: Patentin Ver. 2.0
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Pred. No. 2.1e-57;
0; Mismatches 6;
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; Sequence 210, Application US/09564805
; Patent No. 6333403
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Patent No. 6333403
GENERAL INFORMATION:
APPLICANT: Teng, David H.F.,
APPLICANT: Simard, Jacques,
APPLICANT: Rommens, Johanna M.
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; LOCATION: (51)..(293)
US-09-564-805-210
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Best Local Similarity
Matches 251; Conserv
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ORGANISM: Homo
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Patent No. 6262333
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                           David H.F
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Matches 245; Conservative
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LCCATION: (51)..(29S)

CTHER INFORMATION: exon 1

US-09-564-805-4
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APPLICANT: Myriad Genetics, Inc.

TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility
TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes
FILE REFERENCE: 2318-258
CURRENT APPLICATION NUMBER: US/09/564,805
CURRENT FILING DATE: 2000-05-05
PRIOR FILING DATE: 1998-11.06
PRIOR FILING DATE: 1998-11.06
PRIOR FILING DATE: 1998-11.05
NUMBER OF SEQ ID NOS: 240
SOFTWARE: Patentin Ver: 2.0
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NAME/KEY: misc feature
LOCATION: (910). (13104)
CUHER INFORMATION: exon 1: 910-1154; exon 2: 1736-1786; exon 3:
OTHER INFORMATION: exon 6: 5582-5650; exon 7: 7075-7194; exon 8:
OTHER INFORMATION: 8186-8244; exon 9: 12878-12936; exon 10:
OTHER INFORMATION: 8186-8244; exon 9: 12878-12936; exon 10:
NAME/KEY: misc feature
'OCATION: (13756)..(22917)
'OCATION: (13756)..(22917)
'OCATION: (13756)..(22917)
'OCATION: (13756)..(22917)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: (13756)..(22917)
OTHER INFORMATION: exon 11: 13756-13868; exon 12: 15283-15378; exon OTHER INFORMATION: 13: 16278-16416; exon 14: 16498-16583; exon 15: 0THER INFORMATION: 18583-18701; exon 16: 20349-20345; exon 17: OTHER INFORMATION: 22172-22310; exon 18: 22879-22917
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 CGCACGCGAGAGAAGCGCGGACCGTCGGGGTGCTCCGGCGGCCCCAAACACCGTGTACCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4; Length 26664;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10.0%; Score 247.4; DB 4 97.7%; Pred. No. 2.1e-56; live 0; Mismatches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 4, Application US/09564805
Patent No. 6333403
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             241 AACCGGTATCTCTTCAA 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 97.7
Matches 251; Conservative
                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                    LENGTH: 26664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 8
US-09-564-805-4
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APPLICANT: Rommens, Johanna M.
APPLICANT: Rommens, Johanna M.
APPLICANT: Rommens, Johanna M.
TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility
TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility
TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes
FILE REPERBENCE: 2318-258
CURRENT APPLICATION NUMBER: US/09/564,805
CURRENT FILING DATE: 2000-05-05
PRIOR FILING DATE: 1998-11-06
PRIOR FILING DATE: 1998-11-06
PRIOR FILING DATE: 1998-11-05
NUMBER OF SEQ ID NOS: 240
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CAGGTGGTGGCAGCGGGTAGCCGGGCGCCCCCCCCTCTACGTCTTCTCCGAGTTC 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CGCACGCGAGAGAAGCGCGGACCGTCGGGGTGCTCCGGCGGCGCCCAAACACCGCGTTACCTG 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 51 ATGTGGGCGCTTTGCTCGCTGCTGCGGTCCGCGGCCGGGACGCACCATGTCGCAGGGACGC 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 ACCATATCGCAGGCACCCGCCCGCGGGGGGGGCGCGCAAGGACCCGCTGCGGCACCTG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CGCACGCGAGAGAGCGCGGACCGTCGGGGTGCTCCGGCGGCCCAAACACGCGTGTACCTG 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 ATGTGGGCGCTTTGCTCGCTGCTGCGGTCCGCGGCCGGACGCACCATGTCGCAGGGACGC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9.9%; Score 245; DB 4; Length 295;
100.0%; Pred. No. 8.6e-57;
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APPLICANT: Steinmann, Kathleen E.
APPLICANT: Steinmann, Kathleen E.
APPLICANT: Steinmann, Kathleen E.
APPLICANT: Burgess, Christopher C.
APPLICANT: Bushnell, Steven E.
APPLICANT: Carroll III, Eddie
APPLICANT: Catino, Theodore J.
APPLICANT: Derti, Adnan
APPLICANT: Derti, Adnan
APPLICANT: Lewis, Marcia E.
APPLICANT: Lewis, Marcia E.
APPLICANT: Schlegel, Robert
TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
TITLE OF INVENTION: NOVEL HUMAN GENES
TITLE OF INVENTION: NOVEL HUMAN GENES
TITLE REFERENCE: COLD-257 (US)
CURRENT APPLICATION NUMBER: US/09/128,111
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TYPE: DNA ORGANISM: Homo sapiens
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APPLICANT: Tavigian, Sean V.
APPLICANT: Tavigian, Sean V.
APPLICANT: Teng, David H.F.
APPLICANT: Simard, Jacques
APPLICANT: Simard, Jacques
APPLICANT: Romens, Johanna M.
APPLICANT: Romens, Johanna M.
APPLICANT: Romens, Johanna M.
APPLICANT: Romens, Johanna M.
APPLICANT: Romens, Johanna M.
APPLICANT: Romens, Johanna M.
APPLICANT: Romens, Johanna M.
APPLICANT: Romens, Johanna M.
APPLICANT: NOW Gene and a Paralog and Orthologous Genes
FILE REFERENCE: 2118-258
CURRENT APPLICATION NUMBER: US/09/564,805
CURRENT FILING DATE: 1998-11-06
PRIOR APPLICATION NUMBER: US/0434,382
PRIOR APPLICATION NUMBER: 09/434,382
PRIOR APPLICATION NUMBER: 09/434,382
NUMBER OF SEQ ID NOS: 240
SOFTWARE: Patentin Ver: 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 AGTTAAAGGTTGCTCGCCTGGACAACATATTCCTGACAAGGAATGCACTGGTCTAATGTTG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                 236 AGTICAACCGGIAICTCTICAACTGIGGAGAAGGCGTICAGAGACTCATGCAGGAGCACA 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 AGTICAACCGGTATCTTCTACTGTGGAGAAGGCGTTCAGAGACTCATGCAGGAGCACA 120
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                                                                                                                                                                                                                                                                                                                                      176 ACCTGCAGGTGGCAGCGGGTAGCCGGGACTCGGGCGCCGCGCCTCTACGTCTTCTCCG
                                                                                                                                                                                                                                           Length 238;
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                                                                                                                                                                                                                                         9.6%; Score 237; DB 4; I
100.0%; Pred. No. 1.1e-54;
tive 0; Mismatches 0;
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100.0%; Pred. No. 5.1e-52;
iive 0; Mismatches 0;
EARLIER APPLICATION NUMBER: US 60/088,801
EARLIER FILING DATE: 1998-06-10
NUMBER OF SEQ ID NOS: 850
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 315
LENGTH: 238
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; LOCATION: (1)...(228)
; OTHER INFORMATION: exon 24;
; NAME/KEY: polyA_signal
; LOCATION: (546)...(641)
US-09-564-805-27
                                                                                                                                                                                                                                           Query Match 9.6%
Best Local Similarity 100.0°
Matches 237; Conservative
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Best Local Similarity 100
Matches 228; Conservative
                                                                                                                                              ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-328-111-315
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US-09-564-805-27
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y Depolicant Autonomiation, Sean V.
APPLICANT: Tavtigian, Sean V.
APPLICANT: Tavtigian, Sean V.
APPLICANT: Tavtigian, Sean V.
APPLICANT: Simard, Jacques
APPLICANT: Simard, Jacques
APPLICANT: Myriad Genetics, Inc.
APPLICANT: Myriad Genetics, Inc.
TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility
TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility
TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility
TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility
TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility
CURRENT APPLICATION NUMBER: US 60/107,468
PRIOR FILING DATE: 1998-11-05
PRIOR FILING DATE: 1998-11-05
PRIOR FILING DATE: 1999-11-05
SOUTHWARE: PatentIn Ver. 2.0
SEQ ID NO 26
LENGTH: 145
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Patent No. 6333403
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Tavtigian, Sean V.
APPLICANT: Teng, David H.F.
APPLICANT: Simard, Jacques
APPLICANT: Rommens, Johanna M.
APPLICANT: Myriad Genetics, Inc.
TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility
TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes
FILE REFERENCE: 2318-258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2109 CACAACGTCCCAAGCCATCAGCGTGGGGATGCGGATGAACGCGGAGTTCATTATGCTGAA 2168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2169 CCACTICAGCCAGCGCTAIGCCAAGGICCCCCTCTICAGCCCCAACTICAGCGAGAAAGT 2228
121 ececcercererecadeaderecadecadecadeceredadearecadeadeceredadade 180
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                                                                                                     2374 GCGGCCCTCCTGTCCAGGGAGCTGGCAGCGGCCTGGAGGATGGGGAGCCTCAGCAGAAG
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100.0%; Pred. No. 6e-30; .
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                      2434 CGGCCCACACAGAGGAGCCACAGGCCAAGAAGGTCAGAGCCCCAGTGA 2481
                                                                                                                                                                                                                                                                        181 CGGGCCCACACAGAGGCCACAGGCCAAGAAGGTCAGAGCCCAGTGA 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2229 GGGAGTTGCCTTTGACCACATGAAG 2253
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; Sequence 26, Application US/09564805
; Patent No. 6333403
; GENERAL INFORMATION;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.0
Matches 145; Conservative
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LOCATION: (1)...(145)
CTHER INFORMATION: exon 23
US-09-564-805-26
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GENERAL INFORMATION:
APPLICANT: Tavtigian, Sean V.
APPLICANT: Tavtigian, Sean V.
APPLICANT: Tavtigian, Sean V.
APPLICANT: Simard, Jacques
APPLICANT: Simard, Jacques
APPLICANT: Rommens, Johanna M.
APPLICANT: Rommens, Johanna M.
APPLICANT: Myriad Genetics, Inc.
TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes
FILE REFERENCE: 2318-258
CURRENT APPLICATION WHRER: US/09/564,805
CURRENT APPLICATION NUMBER: US 60/107,468
PRIOR APPLICATION NUMBER: US 994-31-06
PRIOR APPLICATION NUMBER: 09/434,382
PRIOR FILING DATE: 1999:11-05
NUMBER OF SEQ ID NOS: 240
SEQ ID NO 24
LENGTH: 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Tavigian, Sean V.
APPLICANT: Tavigian, Sean V.
APPLICANT: Teng, David H.F.
APPLICANT: Teng, David H.F.
APPLICANT: Simard, Jacques
APPLICANT: Rommens, Johanna M.
APPLICANT: Myriad Genetics, Inc.
TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility
TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes
FILE REFERENCE: 2318-258
CURRENT APPLICATION NUMBER: US/09/564,805
CURRENT FILING DATE: 2000-05-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1969 TCTGGCTGGAAAGTGGTCTATTCCGGGGACACCATGCCCTGCGAGGCTCTGGTCCGGATG 2028
                                    TTACGGAGACCAGGTGGACAGGGTCCTGGGCACCCTGGCTGCTGTTTTGTGTGTCCCACCT 1640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 TTACGGAGACCAGGTGGACAGGGTCCTGGGCACCCTGGCTGCTGTTTGTGTTTGTGTCCCACCT 120
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US-09-564-805-24
: Sequence 24, Application US/09564805
; Patent No. 6333403
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                                                                                                                                    1641 GCACGCAGATCACCACACG 1659
                                                                                                                                                                           121 GCACGCAGATCACCACG 139
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Best Local Similarity 100.0
Matches 121; Conservative
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LOCATION: (1)...(121)

COTHER INFORMATION: exon 21

US-09-564-805-24
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APPLICANT: Tavtigi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 15
US-09-564-805-10
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APPLICANT: Tavtigian, Sean V.
APPLICANT: Teng, David H.F.
APPLICANT: Simard, Jacques
APPLICANT: Simard, Jacques
APPLICANT: Simard, Jacques
APPLICANT: Rommens, Johanna M.
APPLICANT: Rommens, Johanna M.
APPLICANT: Rommens, Johanna M.
APPLICANT: Myriad Genetics, Inc.
TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility
TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes
FILE REFERENCE: 2318-258
CURRENT APPLICATION NUMBER: US/09/564,805
CURRENT APPLICATION NUMBER: US 60/107,468
FRIOR APPLICATION NUMBER: US/434,382
PRIOR FILING DATE: 1999-11-05
NUMBER OF SEQ ID NOS: 240
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 20
LENGTH: 139
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100.0%; Pred. No. 2.5e-28;
tive 0; Mismatches 0;
CURRENT APPLICATION NUMBER: US/09/564,805
CURRENT FILING DATE: 2000-05-05
PRIOR APPLICATION NUMBER: US 60/107,468
PRIOR PILING DATE: 1998-11-06
PRIOR PILING DATE: 1999-11-05
NUMBER OF SEQ ID NOS: 240
NUMBER OF SEQ ID NOS: 240
SEQ ID NO 16
LENGTH: 139
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Patent No. 6333403
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Matches 139; Conservative
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; OTHER INFORMATION: exon 17
US-09-564-805-20
                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc_feature
i_CCATION: (1)..(139)
CTHER INFORMATION: exon 13
US-09-564-805-16
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Matches 139; Conservative
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ORGANISM: Homo sapiens
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LOCATION: (1)..(139)
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ORGANISM: Homo sapiens
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APPLICANT: Tavtigian, Sean V.
APPLICANT: Tavtigian, Sean V.
APPLICANT: Tavtigian, Jacques
APPLICANT: Simard, Jacques
APPLICANT: Simard, Jacques
APPLICANT: Simard, Jacques
APPLICANT: Rommens, Johanna M.
APPLICANT: Rommens, Johanna M.
APPLICANT: Rommens, Johanna M.
APPLICANT: Rommens, Johanna M.
APPLICANT: Rommens, Johanna M.
APPLICANT: Myriad Genetics, Inc.
TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes
FILE REFERENCE: 218-258
CURRENT APPLICATION NUMBER: US/09/988,626
CURRENT APPLICATION NUMBER: US/69/88,626
FRIOR FILING DATE: 2000-05-05
FRIOR PRILING DATE: 1999-11-06
FRIOR FILING DATE: 1999-11-05
FRIOR FILING DATE: 1999-11-05
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US-09-988-626-16

US-09-988-626-10

US-09-988-626-10

US-09-988-626-24

US-09-988-626-14

US-09-988-626-12

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ORGANISM: Homo sapiens
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Sequence 3, Appli
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                              GenCore version 5.1.5
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-988-626-210
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Gapop 10.0 , Gapext 1.0
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ò	1861 GT(SGAAAGATTGATCAGTTCGCTGTTGCGAACATGTGGAAGAGTTTCAGACCTGT 1920
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٥٧	1921 CTC	GGGGGGCACTGCAAGCATGCGTTTGCCTGTGCGCTGGTGCACACTCTGGCTGG
QQ		SGTGCGGCACTGCAAGCATGCGTTTGGCTGTGCGCTGGTGCACCTCTGGCTGG
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qq	1981 GTC	SGTCTATTCCGGGGACACCATGCCCTGCGAGGTTCTGGTCCGGATGGGGAAAGATGCC 2040
Qy	2041 ACC	CCTCCTGATACATGAAGCCACCTGGAAGATGCTTTGGAAGAGGGAAGCAGTGGAAAAG 2100
QQ	2041 ACC	CCTCCTGATACATGAAGCCACCCTGGAAGATGGTTTGGAAGAGGAAGCAGTGGAAAAG 2100
òy	2101 AC	ACACAGCACAACGTCCCAAGCCATCAGCGTGGGGATGAACGCGGGAGTTCATT 2160
qq	2101 AC	ACACAGCACAACGTCCCAAGCCATCAGCGTGGGGGATGCGGATGAACGCGGAGTTCATT 2160
ò	2161 ATC	GONGAACCACTICAGCCAGCGCTATGCCAAGGTCCCCCTCTTCAGCCCCAACTTCAGC 2220
qa	2161 ATC	scrgaaccactrcagccagcgcrargccaaggrccccrtrrcagccccaactrcagc 2220
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APPLICANT: Rommens, Johanna M.

TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility

TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes

FILE REFERENCE: 2318-258

CURRENT APPLICATION NUMBER: US/09/988,687

CURRENT APPLICATION NUMBER: US 60/107,468

PRIOR FILING DATE: 1998-11-06

PRIOR FILING DATE: 1998-11-06

PRIOR APPLICATION NUMBER: 09/434,382

PRIOR APPLICATION NUMBER: 09/434,382

PRIOR APPLICATION NUMBER: 09/434,382

SEQIEN NUMBER OF SEQIEN NO.: 2.0

SOFTWARE: Patentin Ver. 2.0
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ORGANISM: Homo sapiens
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1 UCHER INFORMATION: coding sequence as in SEQ
US-09-988-626-3
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100.0%; Pred. No. 0;
live 0; Mismatches
                                                               ; Sequence 3, Application US/09988626; Publication No. US20030044959A1; GENERAL INFORMATION:
 2461 AAGAAGGTCAGAGCCCAGTGA 2481
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APPLICANT: Tavtiglan, Sean V.
APPLICANT: Tavtiglan, Sean V.
APPLICANT: Tavtiglan, Sean V.
APPLICANT: Tavtiglan, Jacques
APPLICANT: Simard, Jacques
APPLICANT: Rommens, Johanna M.
APPLICANT: Rommens, Johanna M.
TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility
ITILE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility
ITILE OF INVENTION: Gene and a Paralog and Orthologous Genes
FILE REFRENCE: 2318-258
CURRENT APPLICATION NUMBER: US/09/988,626
CURRENT FILING DATE: 2001-11-20
PRIOR APPLICATION NUMBER: US 60/107,468
PRIOR APPLICATION NUMBER: US 60/107,468
PRIOR FILING DATE: 1998-11-06
PRIOR FILING DATE: 1998-11-05
NUMBER OF SEQ ID NOS: 240
SEQ ID NO SEQ ID NOS: 220
SEQ ID NO SEQ ID NOS: 220 470 240 AACCGGTATCTTCTAACTGTGGAGAAGGCGTTCAGAGACTCATGCAGGAGCACAAGTTA 300 360 410 420 480 51 ATGTGGGCGTTTGCTCGCTGCTGCGGCCGGGCGGACGCACCATGTCGCAGGGACGC 110 ACCATATCGCAGGCACCCGCCCCGCGGGGGGGCCGCGAAGGACCCGCTGCGGCACCTG 120 CGCACGCGAGAGAGCGCGGACCGTCGGGGGTGCTCCGGCCGCACAACACGCGTGTACCTG CGCACGCGAGAGAGAGCGCGGACCGTCGGGGTGCTCCGGCGGCCCAAACACCGTGTACTG CAGGIGGIGGIGGCAGCGGGTAGCCGGGACTCGGGCCGCCGCCTCTACGTCTTCTCCGAGTTC CAGGTGGTGGCAGCGGGTAGCCGGGACTCGGGCGCCCGCGCTCTACGTCTTCTCCGAGTTC AAGGTTGCTCGCCTGGACAACATATTCCTGACAACGAATGCACTGGTCTAATGTTGGGGGC AAGGTTGCTCGCCTGGACAACATATTCCTGACACGAATGCACTGGTCTAATGTTGGGGGC TTAAGTGGAATGATTCTTACTTTAAAGGAAACCGGGCTTCCAAAGTGTGTACTTTCTGGA rraagiggaargarrcriactiraaaggaaaccgggcriccaaagrgigtactircrga CCTCCACAACTGGAAAATACCTCGAAGCAATCAAAATATTTTCTGGTCCATTGAAAGGA CCTCCACAACTGGAAAAATACCTCGAAGCAATCAAAATATTTTCTGGTCCATTGAAAGGA .. 0 Length 2958 ATGTGGGCGCTTTGCTCGCTGCGGTCCGCGGCCGGACGCACCATGTCGC Indels 6 ..

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1611 TTTGGGCAGCTGGCGTCATT 1621 GCTGTGTTTGTCCCACCTGC 1631 CAGAGAGAGCGCCTTGGCAT 1731 CAGAGAGAGACGCGCTTGGCAT 1731 CAGAGAGAGACGCGCTTGGCAT 1731 CCCAACCAGCTCTAAGCCTGGCAT 1801 CACACCAGCTCAAGCCTGGCAT 1801 CACACCAGCTCAAGCCTGGCAT 1801 CACACCAGCTCAAGCCTGGCAT 1801 CACACCAGCTCAAGCTTGCCAGCAT 1801 CACACCAGCTCAAGCTTGCCAGCAT 1921 GTGGAAAGATTGATCAGTTCCGCAT 1931 GTGGTCTATTCCGGGGACACCACACACGCACCAGCACACACA	Oy 2461 AAGAAGGTCAGAGCCCAGTGA 2481 Db 2511 AAGAAGGTCAGAGCCCAGTGA 2531	RESULT 4 US-09-080-687-3 ; Sequence 3, Application US/09986687 ; Publication No. US20030045704A1 ; GENERAL INFORMATION: ; APPLICANT: Tavigian, Sean V. ; APPLICANT: Teng, David H.F. ; APPLICANT: Simard, Jacques ; APPLICANT: Rommens, Johanna M. ; APPLICANT: Myriad Genetics, Inc.
	CAGGAGTACAGGAGGAGGAGGACGAGCCCAGCCCAGCAGAGAAAGAAG	1441 CCAGAANTCATTACCTTGGAACAGGGTCTGCCATCCCGATGAAGATTCGAANTGTCAGT 1500

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Oy Op	1621 GCTGTGTTTGTGTCCCACCTGCACGCAGATCACCACACGGGCTTGCCAAGTATCTTGCTG	1680
QQ QD	1681 CAGAGAGAACGCGCCTTGGCAICTTTGGGAAAGCCGCTTCACCCTTTGCTGGTGGTTGCC	1740
oy d	1741 CCCAACCAGGTCAAAGCCTGGCTCCAGGAACCACAACCAGGGGGGGG	1800
OY Dp	y 1801 CACATCAGTATGATTCCTGCCAAATGCCTTCAGGAGGGCTGAGATCTCCAGTCCTGCA	1860
S S	y 1861 GTGGAAAGATTGATCAGTTCGCTGTTGCGAACATGTGATTTGGAAGAGTTTCAGACCTGT 	1920
oy Dp	y 1921 CTGGTGCGGGACTGCAAGCATGCGTTTGGCTGTGCGCTGGTGCACCTCTGGCTGG	1980
oy og	y 1981 GTGGTCTATTCCGGGGACACCATGCCCTGCGAGGCTCTGGTCCGGATGGGGAAAGATGCC	2040
oy Op	2041 ACCCTCCTGATACATGAAGCCACCCTGGAAGATGGTTTGGAAGAAGGAAG	2100
oy og	2101 ACACACAGCACAACGTCCCAAGCCATCAGCGTGGGGATGCGGATGACGCGGAGTTCATT	2160
oy g	y 2161 ATGCTGAACCACTTCAGCCGGGCTATGCCAAGGTCCCCCTCTTCAGCCCCAACTTCAGC	2220
oy og	y 2221 gagaaagtgggaagttgcctttgaccacatgaaggtctgctttggagactttccaacaatg 	2280
8 8	2281 CCCAAGCTGATTCCCCCACTGAAAGCCCTGTTTGCTGGCGACATCGAGGAGATGGAGGAGAGAGTGCTGAGGAGATGCTGAGGAGATGCTGAGGAGAGCCCTGTTTGCTGGCGACATCGAGGAGATGGAGGAG	2340
Q P	2341 CGCAGGAGAAAGCGGGAGCTGCGGCAGGTGCGGGCGCCCTCCTGTCCAGGGAGCTGGCAAACGGGAGCTGCCAGGCAGG	2400
S S	y 2401 GGCGGCCTGGAGGATGGGGAGCCTCAGCAGAAGCGGGCCCACACAGAGGGGCCCACAGAGGGGCCCACACAGAGCGGGCCCACACAGAGCGGGCCCACAGAGCGGGCCCACAGAGCGGGCCCACAGAGCGGGCCCACAGAGCGGGCCCACAGAGCGGGCCCACAGAGCGGGCCCACAGAGCGGGCCCACAGAGCGGGCCCACAGAGCGGGCCCACAGAGCGGGCCCACAGAGCGGGCCCACAGAGCGGGCCCACAGAGCGGGCCCACAGAGCGGGCCCACAGAGCGGGCCCACAGAGCGGGCCCACAGAGCCGAGAGCGGGCCCACAGAGCGGGCCCACAGAGCGGGCCCACAGAGCGGGCCCACAGAGCGGGCCCACAGAGCGGGCCCACAGAGCGGGCCCACAGAGCGGGCCCACAGAGCGGGCCCACAGAGCGGGCCCACAGAGCGGGCCCACAGAGCGGGCCCACAGAGCGGGCCCACAGAGCGGGCCCACAGAGCGGGCCCACAGAGCGGGCCCACAGAGCGGGCCCACAGAGCGGGCCCACAGAGCGGGCCCACACAGAGCCACACAGGCCCCACACAGAGCGGGCCCCACAGAGCGGGCCCCACAGAGCGGGCCCACACAGAGCCGACACAGAGCGGGCCCACACAGAGCGGGCCCACACAGAGCGGGCCCCACACAGAGCGGGCCCACACAGAGCGGGCCCCACACAGAGCGGGCCCCACACAGAGCGGGCCCCACACAGAGCGGGCCCCACACAGAGCGGCCCCACACAGAGCGGGCCCCACACAGAGCGGGCCCCACACAGAGCGGGCCCCACACAGAGCGGGCCCCACACAGAGCGGGCCCCACACAGAGCGGCCCCACACAGAGCGGCCCCACACAGAGCGGGCCCCACACAGAGCGGCCCCACACAGAGCGGCCCCACACACACACACACACACACACACACACACACACAC	2460
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CCCAACCAGCTCAAAGCCTGGCTCCAGCAGTACCACAACCAGTGCCAGGAGGTCCTGCAC 1850
      GAGCCACACCTTCCACATGGTGTTAGCCAGAGAAGAGGGGGTCAGGGACTCTTCCCTGGTC 770
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TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility
TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes
FILE REFERENCE: 2318-258
CURRENT APPLICATION NUMBER: US/09/988,687
CURRENT FILING DATE: 2001-11-20
PRIOR APPLICATION NUMBER: US/054,805
PRIOR APPLICATION NUMBER: US 60/107,468
PRIOR APPLICATION NUMBER: US 60/107,468
PRIOR PILING DATE: 1998-11-05
PRIOR PLILING DATE: 1998-11-05
PRIOR FILING DATE: 1999-11-05
NUMBER OF SEQ ID NOS: 240
SOFTWARE: Patentin Ver: 2.0
SEQ ID NO 3
LENGTH: 2958
TYPE: DNA
ORGANISM: Homo sapiens
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LOCATION: (51). (2531)
OTHER INFORMATION: coding sequence as in SEQ ID NO:1
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; LENGTH: 2908

; TYPE: DNA

; ORCANISM: Pan troglodytes

; FEATURE:

; NAMEX/KEY: CDS

; LOCATION: (1)..(2478)

US-09-988-626-223
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Sequence 223, Application US/09988626

Publication No. US20030044959A1

GENERAL INFORMATION:

APPLICANT: Tavtigian, Sean V.

APPLICANT: Tavtigian, Sean V.

APPLICANT: Tavtigian, Sean V.

APPLICANT: Tavtigian, Sean V.

APPLICANT: Tavtigian, Sean V.

APPLICANT: Tavtigian, Sean V.

APPLICANT: Romens, Johanna M.

APPLICANT: Romens, Johanna M.

APPLICANT: Myriad Genetics, Inc.

ITILE OF INVENTION: Gene and a Paralog and Orthologous Genes

FILE REFERENCE: 2318-258

CURRENT APPLICATION NUMBER: US/09/988,626

CURRENT FILING DATE: 2001-11-20

PRIOR APPLICATION NUMBER: US 60/107,468

PRIOR APPLICATION NUMBER: US 60/107,468

PRIOR FILING DATE: 1999-11-06

PRIOR REDICATION NUMBER: 09/434,382

PRIOR FILING DATE: 1999-11-05

NUMBER OF SEQ ID NOS: 240

SOFTWARE: PatentIn Ver. 2.0
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Query Match
99.0%; Score 2455.4;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 2465; Conservative 0; Mismatches
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APPLICANT: Targivanilow:
APPLICANT: Targivanilow:
APPLICANT: Teng, David H.F.
APPLICANT: Simard, Jacques
APPLICANT: Simard, Jacques
APPLICANT: Simard, Jacques
APPLICANT: Simard, Jacques
APPLICANT: Myriad Genetics, Inc.
TITLE OF INVENTION: Cene and a Paralog and Orthologous Genes
TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes
TITLE REFERENCE: 218-258
CURRENT APPLICATION NUMBER: US/09/988,687
CURRENT FILING DATE: 2000-05-05
PRIOR APPLICATION NUMBER: US 60/107,468
PRIOR FILING DATE: 1998-11-06
PRIOR APPLICATION NUMBER: US 60/107,468
PRIOR FILING DATE: 1999-11-05
NUMBER: O SEQ ID NOS: 240
SEQ ID NO 223
LENGTH: 2908
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Pred. No. 0;
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Best Local Similarity 99.4%;
Matches 2465; Conservative (
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APPLICANT: Tavtigian, Sean V.
APPLICANT: Tavtigian, Sean V.
APPLICANT: Rommens, Johanna M.
APPLICANT: Rommens, Johanna M.
TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility
TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes
TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes
TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes
CURRENT APPLICATION NUMBER: US/09/988,626
CURRENT APPLICATION NUMBER: US/64/805
PRIOR FILING DATE: 2000-05-05/64/805
PRIOR FILING DATE: 1998-11-06
PRIOR FILING DATE: 1998-11-06
PRIOR APPLICATION NUMBER: 09/434,382
PRIOR FILING DATE: 1999-11-05
NUMBER OF SEQ ID NOS: 240
SSEQ ID NO 225
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Pred. No. 0;
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Best Local Similarity 99.0
Matches 2457; Conservative
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LOCATION: (1)
US-09-988-687-225
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APPLICANT: Tartigian, Sean V.
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APPLICANT: Tartigian, Sean V.
APPLICANT: Simadd, Jacques
APPLICANT: Myriad Genetics, Inc.
TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility
TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes
TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes
TITLE OF INVENTION: Cance and a Paralog and Orthologous Genes
TITLE OF INVENTION: Cance and a Paralog
FILE REFERENCE: 2318-258
CURRENT APPLICATION NUMBER: US/09/988,687
PRIOR PILING DATE: 1099-11-05
PRIOR PILING DATE: 1999-11-05
PRIOR PILING DATE: 1999-11-05
PRIOR FILING DATE: 1999-11-05
PRIOR FILING DATE: 1999-11-05
SOFTWARE: Patentin Ver. 2.0
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 225
LENGTH: 2892
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us-09-434-382-1.rnpb

Db 1501 GCCACACTTGTCAAC	1561	1621	1681	1741	1801	1861	1921 CIGGIGCGCA 	1981	2041	2101	2161	2221	2281	2341	2401	Qy 2461 AAGAAGGTCAGAGCCC 	RESULT 9 US-09-988-626-221 ; Sequence 221, Application	; FUBLICATION NO. USZUGJO ; GENERAL INFORMATION: ; APPLICANT: Tavtigian, (
DD 421 CCTCCACAGCTGGAAAAATACCTCGAAGCAATCAAAATATTTTCTGGTCCATTGAAAGA 480	QY 481 ATAGAACTGGCGCCCCACTCTGCCCCAGAATACGAGGATGAAACCATGACAGTT 540 DD 481 ATAGAACTGGCTGTGCGGCCCCACTTGCCCCCAGAATACGAGGATGAAACCATGACATT 540	OY 541 TACCAGATCCCCATACACAGTGAACAGAGGGAAAGCACCAACCA	OY 601 GAAAGGCCTCTCAGCAGGCTCAGTCCAGAGCGATCTTCAGACTCCGAGTCGAATGAAAAT 660	OY 661 GAGCCACACCTTCCACATGGTGTTAGCCAGAGAAGAGGGGTCAGGGACTCTTCCCTGGTC 720	OY 721 GTAGCTTTCATCTGAAGCTTCACTTAAAGAGAGGAAACTTCTTGGTGCTCAAAGCAAAG 780	OY 781 GAGATGGGCCTCCCAGTTGGGACAGCTGCCATCGTCATGCTGCTGTCAAGGAC 840	OY 841 GGGAAAAGCATCACTCATGAAGGAAGAGATTTTGGCTGAAGAGCTGTGTACTCCTCCA 900	OY 901 GATCCTGGTGTTTTGTGGTGGAATGTCCAGATGAAGCTTCATTCA	OY 961 TGTGAGAATGCCACCTTTCAGAGGTACCAAGGAAAGGCAGATGCCCCCGTGGCCTTGGTG 1020	OY 1021 GTTCACATGGCCCCAGCATCTGTGCACAGCAGCAGCAGCACAGCAGTGGATGGA	QY 1081 TTTGGGCCTGACACCCAGCACTTGGTCCTGAATGAGAACTGTGCCTCAGTTCACAACCTT 1140 Db 1081 TTTGGGCCTGACACCCAGCACTTGGTCCTGAATGAGAACTGTGCCTCAGTTCACAACCTT 1140	OY 1141 CGCAGCCACAAGATTCAAACCCAGGTCAACCTCATCCACCGGACATCTTCCCCCTGCTC 1200	OY 1201 ACCAGITICCGCIGIAAGAAGAGGCCCCACCCICAGIGGICCCCAIGGITCAGGGIGAA 1260 Db 1201 ACCAGITICCCCIGIAAGAAGAAGGACCCCACCCICAGIGGICCCAIGGITCAGGGIGAA 1260	OY 1261 TGCCTCCTCAAGTACCAGCTCCGTCCCAGGAGTGGCAGGGGGGGG	Qy 1321 TGCAATCCTGAGGAATTCATAGTTGAGGCGCTGCAGCTTCCCAACTTCCAGGAGCGTG 1380	OY 1381 CAGGAGTACAGGAGGAGGAGGAGGAGGGCCCAGCAGAGAAAAGAAGA	OY 1441 CCAGAAATCATCTTGGAACAGGGTCTGCCATCCCGATGAAGATTCGAAATGTCAGT 1500 DD 1441 CCAGAAATCATCTTGGAACAGGGTCTGCCATCCCCATGAAGATTCGAAATGTCAGT 1500	OY 1501 GCCACACTTGTCAACATAAGCCCCGACACGTCTCTCCTACTGGACTGTGGTGAGGGCACA 1560
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1620 1680 1740 1740 2160 2460 1680 1800 1800 1860 1980 2040 2100 2160 2340 CATAAGCCCCGACACGTCTCTGCTACTGGACTGTGGTGAGGGCACG 1560 1920 1920 GGACACCATGCCCTGCGAGGCTCTGGTCCGCATGGGGAAAGATGCC 2040 IGAAGCCACCCTGGAAGAAGATGGTTTGGAAGAAGGAAGCAGTGGAAAAG 2100 2220 CAGCCAGCGCTATGCCAAGGTCCCCCTCTTCAGCCCCAACTTCAAC 2220 2280 cccacreaaaecccrerrrecceeceacarceaeaaareaaeae 2340 2400 GGAGCTGCGGCAGGTGCGGCCCTCCTGTCCGGGGAGCTGGCA 2400 CCGTCATTACGGAGACCAGGTGGACAGGGTCCTGGGCACCCTGGCT CCGTCATTACGGAGACCAGGTGGACAGGGTCCTGGGCACCCTGGCT CCACCTGCACGCAGATCACCACACGGGCTTGCCAAGTATCTTGCTG CTTGGCATCTTTGGGAAAGCCGCTTCACCCTTTGCTGGTGGTTGCC CTTGGCATCTTTGGGAAAGCCCCTTCACCTTTGCTGGTGGTTGCC AGCCTGGCTCCAGCAGTACCACAACCAGTGCCAGGAGGTCCTGCAC AGCCTGGCTCCAGCAGTACCACAACCAGTGCCAGGAGGTCCTGCAC TCCTGCCAATGCCTTCAGGAGGGGCTGAGATCTCCAGTCCTGCA CAGTTCGCTGTTGCGAACATGTGATTTGGAAGAGTTTCAGACCTGT SGACACCATGCCCTGCGAGGCTCTGGTCCGGATGGGGAAAGATGCC TGAAGCCACCCTGGAAGATGGTTTGGAAGAGGAAGCAGTGGAAAAG GTCCCAAGCCATCAGCGTGGGGATGCGGATGAACGCGGAGTTCATT GTCCCAAGCCATCAGCGTGGGATGCGGATGAACGCGGAGTTCATT CAGCCAGCGCTATGCCAAGGTCCCCCTCTTCAGCCCCCAACTTCAGC IGCCTTTGACCACATGAAGGTCTGCTTTGGAGACTTTCCAACAATG CCCACTGAAAGCCCTGTTTGCTGGCGACATCGAGGAGATGGAGGAG SGAGCTGCGGCAGGTGCGGCGCCCTCCTGTCCAGGGAGCTGGCA TGGGGGAGCCTCAGCAGAAGCGGGCCCACACAGAGGAGCCACAGGCC CAGITICGCIGITGCGAACAIGTGAITTGGAAGAGITTCAGACCIGI CAGTGA 2481 CCAGTGA 2481

ion US/09988626 0044959A1 Sean V.

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APPLICANT: Teng, David H.F.

APPLICANT: Simard, Jacques
APPLICANT: Somenes, Johanna M.
APPLICANT: Mornad Genetics, Inc.
TTLLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility
TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes
TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes
TITLE OF INVENTION: Cancer 17p-Linked Prostate Cancer Susceptibility
TITLE OF INVENTION: Cancer 17p-Linked Prostate Cancer Susceptibility
TITLE OF INVENTION: Cancer 17p-Linked Paralog and Orthologous Genes
CURRENT APPLICATION NUMBER: US/09/988,626
CURRENT FILING DATE: 2000-05-06
PRIOR APPLICATION NUMBER: US 60/107,468
PRIOR FILING DATE: 1998-11-06
PRIOR APPLICATION NUMBER: 09/434,382
PRIOR APPLICATION NUMBER: 09/434,382
PRIOR PILING DATE: 1999-11-05
NUMBER OF SEQ ID NOS: 240
SEQ ID NO 221
LENGTH: 2470
TURNEL DATE: 2470
TURNEL DATE: 2470
TURNEL DATE: 2470
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 2470;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
66.3%; Score 1645.6; DB 9; Length
Best Local Similarity 81.6%; Pred. No. 0;
Matches 1958; Conservative 0; Mismatches 417; Indels
                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Mus musculus
FEATURE:
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                                                                                                                                                                                                             CCAGATCCTGGTCTTGTATTCATCGTGGTAGAGTGTCCTGATGAAGGATTCATCCTGCCC 918
                                                                                      AAGGAGCTGGGCCTTCCTGTTGGGACGCCGCCATTGCACCCATCATTGCTGCTGTCAAG 798
                                                                                                                                     GACGGGAAGAGTATCACTTACGAAGGAAGAGAGATTGCTGCTGAAGAGGCTTTGTACACC 858
                                                                                                                                                                                GTGGTCCACATAGCCCCAGAATCTGTACTCATCGACAGCAGATACCAGCAGTGGAG
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                                                         AAGGAGATGGGCCTCCCAGTTGGGACAGCTGCCATCGCTCCCATCATTGCTGCTGTCAAG
                                                                                                                    GACGGGAAAAGCATCACTCATGAAGGAAGAGAGATTTTGGCTGAAGAGCTGTGTACTCCT
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Sequence 221, Application US/09988687

GENERAL INFORMATION:
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APPLICANT: Tartigian, Jacques
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APPLICANT: Myriad Genetics, Inc.
TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility
TITLE OF INVENTION: Chromosome 17p-Linked Prostate Genes
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CURRENT PAPLICATION NUMBER: US/09/988,687
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ORGANISM: Mus musculus
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                                                                                                                                             Score 1645.6; DB 9;
Pred. No. 0;
0; Mismatches 417;
                                                                                                                                             66.3%;
ilarity 81.6%;
Conservative
                                         .. (2466)
                                                                                                                                                Query Match
Best Local Similarity
Matches 1958; Conserv
; NAME/KEY: CDS
; LOCATION: (1)
US-09-988-687-221
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ω ; Acid and Protein Homologs CGGATGAATGCGGAGTTC 2118 CTCTTCAGCCCCAACTTC 2217 |||||| || || crcrgacc---cagcag 2355 CTCCTGTCCAGGGAGCTG 2397 TTCAACTGTGGAGAAGGC 270 |||||||||||||||| TTCAACTGTGGAGAAGGC 179 SAAAATACCTCGAAGCA 450 ; Indels 3; Gaps 0; Length 783;

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181 GTTCAGAGACTCATGCAGGAGCACAAGTTAAAGGTTGCTCGCCTGGACAACATATTCCTG 240
                                                                                                                                   ACCGGCTTCCAAAGTGTGTACTTTCTGGACCTCCACAACTGGAAAAAAACCTCGAAGGA 360
                                                                                                                                                                                                              ATCAAAATTTTTTCTGGTCCATTGAAAGGAATAGAACTGGCTGTGCGGCCCCACTCTGCC 420
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                                                           ACACGAATGCACTGGTCTAATGTTGGGGCTTAAGTGGAATGATTCTTACTTTAAAGGAA
                                                                                                                ACCGGGCTTCCAAAGTGTGTATTTCTGGACCTCCACAACTGGAAAAATACCTCGAAGCA
                                                                                                                                                                                           ATCAAAATATTTTCTGGTCCATTGAAAGGAATAGAACTGGCTGTGCGGCCCCACTCTGCC
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| Publication No. US20030073623A1
| GENERAL INFORMATION: US20030073623A1
| APPLICANT: Hyseq. Inc.
| TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
| TITLE OF INVENTION: FROM VARIOUS cDNA LIBRARIES
| FILE REFERENCE: 20411-756
| CURRENT APPLICATION NUMBER: US/09/918,995
| CURRENT FILING DATE: 2001-07-30
| PRIOR APPLICATION NUMBER: US/09/235,076
| PRIOR PILING DATE: 1999-01-20
| NUMBER OF SEQ ID NOS: 38054
| SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                       CCAGAATACGAGGATGAAACCATGACAGTTTACCAGATCCCCATACACAGTG
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91.3%; Pred. No. 1.6e-125;
live 0; Mismatches 44;
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, OTHER INFORMATION: n = A,T,C or G
US-09-918-995-8996
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Best Local Similarity 91.3
Matches 502; Conservative
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ORGANISM: Homo sapiens
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US-09-918-995-8996
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GENERAL INFORMATION:
APPLICANT: Robison, Keith E.
TITLE OF INVENTION: No. US20020132090Alel Nucleic Acid and Protein Homologs:
FILE REFERENCE: 5800-119
CURRENT FILING DATE: 2001-04-11
FRIOR APPLICATION NUMBER: US/09/833,381
CURRENT FILING DATE: 2000-02-29
NUMBER OF SEQ ID NOS: 2050
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 2038
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300 ACCGGGCTTCCAAAGTGTGTACTTTCTGGACCTCCACAACTGGAAAAATACCTCGAAGCA 359
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                                                       CCAGAATACGAGGATGAAACCATGACAGTTTACCAGATCCCCATACACAGTGAACAGAGG
                                                                                                                                                                                                              480 AGGGGAAAGCACCAACCATGGCAGAGTCCAGAAAGGCCTCTCAGCAGGCTCAGTCCAGAG
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                                                                                                              511 CCAGAATACGAGGATGAAACCATGACAGTTTACCAGATCCCCATACACAGTGAACAGAGG
                                                                                                                                                                                       571 AGGGGAAAGCACCAACCATGGCAGAGTCCAGAAAGGCCTCTCAGCAGGCTCAGTCCAGAG
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                                   451 ATCAAAATATTTTCTGGTCCATTGAAAGGAATAGAACTGGCTGTGCGGCCCCACTCTGCC
                                                                                                                                                                                                                                                                                                                                                                                                                   GAGAGGAAACTTCTTGGTGCTCAAAGCAAAGGAGATGGGCCTCCCCAGTTGGGACAGCTGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 12
8.09-833 281-2038
; Sequence 2038, Application US/0983381
; Patent No. US20020132090A1
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Matches 471; Conservative
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ORGANISM: Homo sapiens
US-09-833-381-2038
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GATTT 783
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Search completed: May 18, 2003, 00:05:36 Job time : 322.542 secs
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Sequence 210, Application US/09988626

Publication No. US20030044959A1

Sequence 210, Application US/09988626

Publication No. US20030044959A1

APPLICANT: Tavtigian, Sean V.

APPLICANT: Tavtigian, Jacques

APPLICANT: Simard, Jacques

APPLICANT: Rommens, Johanna M.

APPLICANT: Myriad Genetics, Inc.

TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility

TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility

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TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility

FILE REFERENCE: 2318-258

CURRENT FILING DATE: 2001-11-20

PRIOR FILING DATE: 1998-11-05

PRIOR FILING DATE: 1998-11-05

PRIOR FILING DATE: 1999-11-05

NUMBER OF SEQ ID NOS: 240

SOFTWARE: PatentIn Ver. 2.0
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ORGANISM: Homo sapiens
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; LOCATION: (51)..(293)
US-09-988-626-210
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JOURNEY BENEARY CALL OF APPLICATION US/09988687

Sequence 210, Application US/09988687

Sequence 210, Application US/09988687

SENERAL INFORMATION:
Sean V.
APPLICANT: Tavididan, Sean V.
APPLICANT: Simard, Jacques
APPLICANT: Rommens, Johanna M.
APPLICANT: Rommens, Johanna M.
APPLICANT: Myriad Genetics, Inc.
TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility
TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes
FILE REFERENCE: 2318-258
CURRENT APPLICATION NUMBER: US/09/988,687
CURRENT FILING DATE: 2001-11-20
PRIOR FILING DATE: 2000-05-05
PRIOR FILING DATE: 1998-11-06
PRIOR PRIOR APPLICATION NUMBER: 09/434,382
PRIOR PRIOR APPLICATION NUMBER: 09/434,382
RIOR FILING DATE: 1999-11-05
NUMBER OF SEQ ID NOS: 240
SEQ ID NO 210
LENGTH: 350
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Pred. No. 2.7e-67;
0; Mismatches 6;
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Best Local Similarity 97.7%;
Matches 251; Conservative C
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    , NAME/KEY: CDS
; LOCATION: (51)..(293)
US-09-988-687-210
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Strausberg,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
Submitted (04-F82-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-romail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
NA Sequencing Center
Sequencing Center
Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
                             BQ064858 R
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AUTHORS
TITLE
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Score

Result No.

Post-processing:

Database

Minimum DB seq Maximum DB seq

Title: Perfect score:

Sequence:

Scoring table:

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Arccgaaargrcagrrccacacrcgrcaaccraagcccrgacaaarcagrgcrccrggar 1548
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 AATGGGCAGTGCCCTCCAGAGGACAGCAGTGCAGGTGCCAACAGGAAAGCATGGGGCAGG
                                                                                                                  CTGTGTACTCCTCCAGATCCTGGTGCTGCTTTTTGTGGTGGTAGAATGTCCAGATGAAAGC
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                                                                             Clone distribution: MGC clone distribution information can be for through the I.M.A.G.B. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 36 Row: o Column: This clone was selected for full length sequencing because it passed the following selection criteria: Similarity but not
                                                                                                                                                                                                                                                                                          /tissue_type="Mammary tumor metastatized to lung. Tumor arose spontaneously from a senescent normal mammary (clonal) outgrowth infected with the virus MMTV." (clone lib="WOIL CGAP_Lu29" /lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    417
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Martin, R.G., Muzny,
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                                                                                                                                                            identity to protein
This clone has the following problem: frame shifted
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                         66.9%; Score 1661; DB 11; Length 81.6%; Pred. No. 0; ive 0; Mismatches 415; Indels
                . . .
                                                                                                                                                                                                                                                                                                                                                                        'note="Vector: pCMV-SPORT6"
771 c 780 g 599 t
Contact: amg@bcm.tmc.edu
dunaratne, P.H., Garcia, A.M., Lu,
Yoon, V.S., Kowis, C.R., Lawrence,
Richards, S., Gibbs, R.A.
                                                                                                                                                                                                                         /organism="Mus musculus"
/db_xref="taxon:10090"
/map="CZECH II"
                                                                                                                                                                                                                                                                             clone="IMAGE:4018447"
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Mus musculus 18 days embryo whole body cDNA, RIKEN full-length
enriched library, clone:111003727:DNA segment, Chr 11, Wayne State
University 80, expressed, full insert sequence.
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Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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AK004136.1 GI:12835201
HTC; CAP trapper.
Mus musculus (strain:C57BL/6J) 18 days embryo cDNA to mRNA,
clone_lib:RIKEN full-length enriched mouse cDNA library
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                              1789 caggagarrergeaceacercagrargarrecreceaaargeerreagaaggeagag
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                                                                 ATCTCCAGTCCTGCAGAGGATTGATCAGTTCGCTGTTGCGAACATGTGATTTGGAA
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/db_xref="MGD.inG1:106352"
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                                                                                                                                                                                              /clone lib="RIKEN full-length enriched mouse cDNA library"
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LVNLSPDKSVLLDCGEGTFGQLCRHYGQQIDRVLCSLTAVFVSHLHADHHTGLLNILL
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GKDATLLIHEATLEDGLEBEAVEKTHSTTSQAINVGMRMNAEFIMLNHFSQRYAKIPL
FSPDFNEKVGIAFDHMKVCFGDFPTVPKLIPPLKALFAGDIEEMVERREKRELRLVRA
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(db_xref="FANTOM DB:1110037C17"

/db_xref="MGD:MGI:190073"

/db_xref="taxon:10090"

/clone="1110037C17"
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                                                                                                                          'organism="Mus musculus"
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/clone="INAGE:8804032"
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EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCACGAG(G). Size-selected >500bp for average insert size
I.8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NIH_MGC
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1030)
                                                                                             Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lou Staudt
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2040 row: p column: 17
High quality sequence stop: 647.
L.1030 Qualifiers
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                                              NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Pred. No. 1.4e-222;
0; Mismatches 13; Indels 3;
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/clone="Inba"NIH_MGC_4"
/clone="Organ: brain; Vector: pOTB%; Site 1: Xhol; Site_2: /note="Organ: brain; Vector: pOTB%; Site 1: Xhol; Site_2: /note="Organ: brain; Vector: potB%; Site 1: Xhol; Site_2: /note="Organ: brain; Vector: potB%; Site 1: Xhol; Site_2: /note = CoNR; coNA made by oligo-dr priming. Directionally cloned into EcoRIX/Khol sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in
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Homo sapiens cDNA clone IMAGE:6339041
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Email: cgapbs-r@mail.nih.gov
Tissue Procourement: Arcc
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2533 row: d column: 18
High quality sequence stop: 699.
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11 (bases 1 to 930)
11H-MGC http://mgc.ncl.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
541 GGCTGAAGAGCTGTGTACTCCTCCAGATCCTGGTGCTTTTGTGGTGGTGGTAGAATGTCC
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901 GCGGCCACACAGAG 914

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the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies) Note: this is a NIH MGC Library." 2 others
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Pred. No. 3.6e-214;
0; Mismatches 17;
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1. 918
/ Organism="Homo sapiens"
/ Organism="Homo sapiens"
/ Ab_refe"=Laxon:9606"
/ Clone=InhaGE:6279B15"
/ Clone lib="NIH MGC 113"
/ Llab_hote="Multo" (pinge-resistant)"
/ Llab_hote="Multo" (pinge-resistant)"
/ Llab_hote="Multo" (pinge-resistant)"
/ Llab_hote="Multo" (pinge-resistant)"
/ Llab_hote="Organ: spleen; Vector: pOTB7; Site 1: XhoI; Site 2:
/ Llab made by oligo-dT priming. Directionally cloned
inco EcoRI; CDNA made by oligo-dT priming. Directionally cloned
inco EcoRI; Abot sites using the following 5' adaptor:
GGCAGGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH MGC Library."
                                         mRNA linear EST 16-JUL-2002 sapiens cDNA clone IMAGE:6279815
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                                                                                                                                                                                                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Mark Matson
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can leound through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
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High quality sequence stop: 625.
Location/Qualifiers
                                              pp dq
                                                               AGENCOURT 8353712 NIH MGC 113
5', mRNA Sequence.
BQ706437
                                              918
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BQ706437
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/organism="Homo sapiens"
/db_xcef="taxon:9606"
/clone="lb="NHMGE.593173"
/clone_lib="NHMGE.99"
/tissue_type="lymphoma.cell line"
/lab_host="DH10B (phage-resistant)"
/lote="Organ: lymph; Vector: pOTB7; Site_1: XhoI; Site_2:
FCORI, cDNA made by oligo-dT priming. Directionally cloned
inco EcoRI/XhoI sites using the following 5' adaptor:
GGCACGAG(G). Size-selected ->5000p for average insert size
inco EcoRI/XhoI sites using the following 5' adaptor:
GGCACGAG(G). Size-selected by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
il RT (Life Technologies). Note: this is a NIH_MGC
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Pred. No. 2.7e-212;
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5', mRNA sequence.
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NIH-MGC http://mgc.nci.nih.gov/.
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lou Staudt
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2112 row: b column: 06
High quality sequence start: 16
High quality sequence stop: 672.
Location/Qualifiers
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LOCUS

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ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL

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/clone="IMAGE:579676"
/clone="IMAGE:579676"
/clone="IMAGE:579676"
/clone="IMAGE:579676"
/tissue type="1ymboma, cell line"
/lab host="DH10B (phage-resistant)"
/lab host="DH10B (phage-resistant)"
/note="Organ: lymph; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
IGGCACGAG(G). Size-selected >500bp for average insert size
1.8Mb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NIH_MGC
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                                                                                                                                                                                                                                                                                                                                       BM927353 1067 bp mRNA linear EST 12-MAR-2002
AGENCOURT 6704919 NIH_MGC_99 Homo sapiens cDNA clone IMAGE:5796765
5', mRNA Sequence.
BM927353 GI:19377732
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I (bases 1 to 1067)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lou Staudt
cDNA Library Preparation: Rubin Laboratory
cDNA Library Preparation: Rubin Laboratory
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2022 row: a column: 22
High quality sequence stop: 650.
Location/Qualifiers
                               1179
                                                                                             1180 CC-GGACATCTTCCCCCTGCTCACCAGTTTCCGCT-GTAAGAAGGAGGGCCCCACCCTCA 1237
                                                                                                                                                            GTGTGCCCATGG-TTCAGGGTGAATGCCTCCTCAAGTACCAGCTCCGTCCCAGGA---GG 1293
                                                                                                                                                                                 GGGGGCCCATGGTTTCAGGGTGAATGCCCTCCTCAGNTACAGCTCCGNTCCAANAAAGGA 989
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                                                                                                                CCGGGACATCTTCCCCCTGCTCACTCCCCCTGGTAAGAAGAGGCCCCCCACCTCA 929
750 ACCAGCAGTGGATGGAGAAGTTTGGGCCTGACACCCCAGCACTTGGTCCTGAATGAGAACT 809
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                                                  810 GTGCCTCAGTTCACAACCTTCGCAGCCACAAGATTCAAACCCCAGGTCAACCTCATCCAC
                               GTGCCTCAGTTCACAACCTTCGCAGCCACAAGATTCAAA.CCCAGCTCAACCTCATCCAC
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34.4%; Score 854.4; DB 14; Length 1067;

Best Local Similarity 97.3%; Pred. No. 1.4e-208;

Matches 880; Conservative 0; Mismatches 21; Indels 3;
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AUTHORS
TITLE
JOURNAL
COMMENT
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KEYWORDS
SOURCE
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915 bp mRNA linear EST 16-AUG-2002
AGENCOURT 8071095 NIH_MGC_112 Homo sapiens cDNA clone IMAGE:6089876
BQ890505
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
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                        61 GCTTCCAAAGTGTGTACTTTCTGGACCTCCACAACTGGAAAAATACCTCGAAGCAATCAA 120
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GCTTCCAAAGTGTGTACTTTCTGGACCTCCACAACTGGAAAAATACCTCGAAGCAATCAA
                                                                                  AATATTTTCTGGTCCATTGAAAGGAATAGAACTGGCTGTGCGGCCCCACTCTGCCCCAGA
                                                                                                                                                                    ATACGAGGATGAAACCATGACAGTTTACCAGATCCCCATACACAGTGAACAGAGGAGGG
                                                                                                                                                                                                 AAAGCACCAACCATGGCAGAGTCCAGAAAGGCCTCTCAGCAGGCTCAGTCCAGAGCGATC
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/tlssue type="melanotic melanotic melanoma skin, Vector: pormer, site_1: XhoI; Site_2:
ECORI; cDNA made by Oilgo-dT priming. Directionally cloned
into ECORI/XhoI sites using the following 5' adaptor:
GGCAGGG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
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                                                                                                       Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2330 row; f column: 21
High quality sequence stop: 720.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 915)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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llarity 99.5%; Pred. No. 1.2e-202;
Conservative 0; Mismatches 4;
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Best Local S:
Matches 833
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ORIGIN
                                                                TITLE
JOURNAL
COMMENT
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
I (bases 1 to 1042)
NIH-MGC http://mgc.nci.nih.gov/.
L Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lou Staudt
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2064 row: f column: 23
High quality sequence stop: 663.
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Pred. No. 5.4e-202;
); Mismatches 22; Indels 6;
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261 c Library."

/organism="Homo sapiens"

source

FEATURES

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 978)

S NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robers Erausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: Lou Staudt

cDNA Library Preparation: Rubin Laboratory

cDNA Library Preparation: Rubin Laboratory

cDNA Library Preparation: Rubin Laboratory

cDNA Library Preparation: Rubin Laboratory

cDNA Library Preparation: Rubin Laboratory

cDNA Library Preparation: Rubin Laboratory

cDNA Library Preparation: Rubin Laboratory

cDNA Library Preparation: Rubin Laboratory

cDNA Library Preparation: Accolned distribution information can be

found through the I.M.A.G.E. Consortium/LiNL at:

http://image.llni.gov

Plate: LiCMX107 row: d column: 17

High quality sequence stop: 620.

Location/Qualifiers

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                                                      14; Length 978
   2 others
                                                                                       Indels
                                                                                       11;
                                                    Query Match
33.1%; Score 821.6; DB 14
Best Local Similarity 98.5%; Pred. No. 3.7e-200;
Matches 849; Conservative 0; Mismatches 11;
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BASE COUNT
ORIGIN
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978 bp mRNA linear EST 02-APR-2002
AGENCOURT 6856603 NIH_MGC_99 Homo sapiens cDNA clone IMAGE:5929312
57, mRNA sequence.
BQ064858
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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BQ064858.1 GI:19893889

LOCUS DEFINITION

RESULT 10 BQ064858 human.

ORGANISM ACCESSION VERSION KEYWORDS SOURCE

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Score 820.8;
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96.4%;
                                               Best Local Similarity 96.4
Matches 894; Conservative
                                  Query Match
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/lab.host="neuroblastoma, vector: poTB7; site 1: XhoI; Site_2: BCORI; cDNA made by ollgo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size=selected 5500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Supersoript II RT (Life Technologies).
Note: this is a NIH MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

B 1 (bases 1 to 970)
S NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
L Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: Gapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Rubin Laboratory
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.llnl.gov
Plate: LLCM2102 row: 1 column: 04
High quality sequence stop: 723.
                                                                                                                                                                                                                                                                                                                                                                                                                                   AČENCOURT_6853053 NIH_MGC_47 Homo sapiens cDNA clone IMAGE:5927571 5', mRNA sequence.
BQ071202.1 GI:19900248
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541 GGCTGAAGAGCTGTGTACTCCTCCAGATCCTGGTGCTGCTTTTGTGGTGGTAGAATGTCC
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AUTHORS
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JOURNAL
COMMENT
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Homo sapiens
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ECORI: cDNA made by oligo-dr priming. Directionally cloned
into EcoRI/Xho1 sites using the following 5' adaptor:
GGCACGAG(G). Size-selected >500bp for average insert size
1.8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
// Life Technologies). Note: this is a NIH_MGC
BUCL9218 1009 bp mRNA linear EST 29-MAR-2002
AGENCOURT 7049753 NIH_MGC_99 Homo sapiens cDNA clone IMAGE:5815225
57, mRNA Sequence.
                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1009)
                                                                                                                                                                                                                             Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: gapbs-remail.nih.gov
Tissue Procurement: Lou Staudt
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information cloud through the I.M.A.G.E. Consortium/LLNL at:
http://mage.llnl.gov
Plate: LLCM2070 row: c column: 02
High quality sequence stop: 682.
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National Institutes of Health, Mammalian Gene Collection (MGC)
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ORIGIN
                             DEFINITION
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                                                                                                                                                                              REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
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AGENCOURT 7054570 NIH_MCC_47 Homo sapiens cDNA clone IMAGE:5922163 5', mRNA sequence.
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/clone="IMAGE:5922163"
/clone=lib="NIH MGC 47"
/tissue_type="neuroblastoma, cell line"
/lab.host="DH108 (phage-resistant)"
/note="Organ: brain; Vector: pOTB7; Site_1: XhoI; Site_2:
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATC
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://inage.llnl.gov
Plate: LLCM2088 row: j column: 20
High quality sequence stop: 675.
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1. (bases 1 to 983)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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ECORI; cDNA made by oligo-dT priming. Directionally cloned into ECORI/XhoI sites using the following 5' addaptor: GGCACGAG(G). Size-selected $500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Strategene) and Superscript II RT (Life Technologies). Note: this is a NIH MGC Library."
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Pred. No. 1.4e-194;
0; Mismatches 36;
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Best Local Similarity 95.2%;
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/organism="Homo sapiens"
/db xref="taxon:9606"
/clone="InAGE:6210029"
/clone="InAGE:6210029"
/clone="InAGE:6210029"
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/clone="InAGE:62100"
/clone="InAGE:62100"
/clone="Organ: pancreas; vector: pOTB7; Site_1: XhOI; Site_2: ECORI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhOI sites using the following 5' adaptor: GGACGAGG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library." I others
                                                                                                                                                               876 bp mRNA linear EST 15-JUL-2002
AGENCOURT_8039759 NIH_MGC_110 Homo sapiens cDNA clone IMAGE:6210029
5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: cgapDs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
DNA Sequencing by: Agencourt Bioscience Corporation
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov column: 06
High quality sequence stop: 708.
Location/Qualifiers
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PAGENCOUNT_8212075 NIH_MGC_112 Homo sapiens cDNA clone IMAGE:6264396
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 928)
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                                          CAGTGCCACATGTCAACATAAAGCCCCCGACACGTCTCTGCTACTGGACTGTGGGGG
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AUTHORS TITLE JOURNAL COMMENT

FEATURES

REFERENCE

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